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DIVISION-CONTINUATION APPLICATION TRANSMITTAL FORM

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Class SubclassPrior Application:
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To the Assistant Commissioner for Patents:

This is a request for filing a ☒ continuation ☐ divisional application, under 37 CFR 1.53(b), of pending prior application
Serial No. 08/880,855 filed on June 23 19 97,
of William J. Boyle
for OSTEOPROTEGERIN BINDING PROTEINS

1. ☒ Enclosed is a copy of the prior application, Serial No. 08/880,855, filed on June 23, 1997
including the oath or declaration as originally filed.
2. ☒ The filing fee is calculated below:

| For | Number Filed | | Number Extra | | Rate | | Fee |
|---------------------------|--------------|--------|--------------|---|----------|---|------------|
| Total Claims | 41 | - 20 = | 21 | x | \$22.00 | = | \$462.00 |
| Independent Claims | 11 | - 3 = | 8 | x | \$82.00 | = | 656.00 |
| Multiple Dependent Claims | 5 | | | + | \$270.00 | = | 270.00 |
| Basic Fee | | | | | \$790.00 | = | 790.00 |
| Total Filing Fee | | | | | | | \$2,178.00 |

3. ☒ The Commissioner is hereby authorized to charge any filing fees which may be required by the accompanying application, any additional fees which may be required during pendency of this application, or credit any over-payment to Deposit Account No. 01-0519 in the name of Amgen Inc. An original and one copy are enclosed.
4. ☐ A check in the amount of \$ _____ is enclosed.
5. ☐ Cancel in this application original claims _____
of the prior application before calculating the filing fee. (At least one original independent claim must be retained for filing purposes.)
6. ☒ Amend the specification by inserting before the first line the sentence:

--This application is a ☒ continuation ☐ division of application Serial No. 08/880,855,
filed June 23, 1997, which is a continuation-in-part of application Serial No. 08/842,842, filed April 16, 1997, now U.S.
Patent No. 5,843,678, which is hereby incorporated by reference.--

EXPRESS MAIL CERTIFICATE

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Date of Deposit

December 14, 1998

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to Box Patent Application, Assistant Commissioner for Patents, Washington, DC 20231.

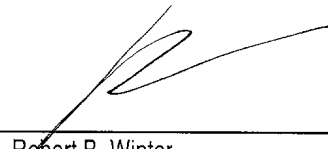
Alan Sorenson

Printed Name

Alan Sorenson

Signature

7. ☐ Transfer the drawings from the prior application to this application and abandon said prior application as of the filing date accorded this application. A duplicate copy of this sheet is enclosed for filing in the prior application file. (May only be used if signed by person authorized by § 1.138 and before payment of base issue fee.)
- 7a. ☐ New formal drawings are enclosed.
8. ☐ Priority of application Serial No. _____ filed on _____ in _____ (country) is claimed under 35 USC 119.
- 8a. ☐ The certified copy has been filed in prior application Serial No. _____ filed _____
9. ☒ The prior application is assigned of record to Amgen Inc.
10. ☐ A preliminary amendment is enclosed.
11. ☐ Also enclosed _____
12. ☐ Other: _____
13. ☒ The power of attorney in the prior application is to:
Ron K. Levy, Registration No. 31,539; Steven M. Odre, Registration No. 29,094;
Robert B. Winter, Registration No. 34,458
- a. ☒ The power appears in the original papers in the prior application.
- b. ☐ Since the power does not appear in the original papers, a copy of the power in the prior application is enclosed.
- c. ☒ Address all future communications to
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OSTEOPROTEGERIN BINDING PROTEINS

Field of the Invention

5 The present invention relates to polypeptides
which are involved in osteoclast differentiation. More
particularly, the invention relates to osteoprotegerin
binding proteins, nucleic acids encoding the proteins,
expression vectors and host cells for production of the
10 proteins, and binding assays. Compositions and methods
for the treatment of bone diseases, such as
osteoporosis, bone loss from arthritis, Paget's disease,
and hypercalcemia, are also described.

15

Background of the Invention

Living bone tissue exhibits a dynamic
equilibrium between deposition and resorption of bone.
These processes are mediated primarily by two cell
20 types: osteoblasts, which secrete molecules that
comprise the organic matrix of bone; and osteoclasts,
which promote dissolution of the bone matrix and
solubilization of bone salts. In young individuals with
growing bone, the rate of bone deposition exceeds the
25 rate of bone resorption, while in older individuals the
rate of resorption can exceed deposition. In the latter
situation, the increased breakdown of bone leads to
reduced bone mass and strength, increased risk of
fractures, and slow or incomplete repair of broken
30 bones.

Osteoclasts are large phagocytic multinucleated
cells which are formed from hematopoietic precursor
cells in the bone marrow. Although the growth and
formation of mature functional osteoclasts is not well

understood, it is thought that osteoclasts mature along the monocyte/macrophage cell lineage in response to exposure to various growth-promoting factors. Early development of bone marrow precursor cells to

5 preosteoclasts are believed to be mediated by soluble factors such as tumor necrosis factor- α (TNF- α), tumor necrosis factor- β (TNF- β), interleukin-1 (IL-1), interleukin-4 (IL-4), interleukin-6 (IL-6), and leukemia inhibitory factor (LIF). In culture, preosteoclasts are

10 formed in the presence of added macrophage colony stimulating factor (M-CSF). These factors act primarily in early steps of osteoclast development. The involvement of polypeptide factors in terminal stages of osteoclast formation has not been extensively reported.

15 It has been reported, however, that parathyroid hormone stimulates the formation and activity of osteoclasts and that calcitonin has the opposite effect, although to a lesser extent.

Recently, a new polypeptide factor, termed

20 osteoprotegerin (OPG), has been described which negatively regulated formation of osteoclasts in vitro and in vivo (see co-owned and co-pending U.S. Serial Nos. 08/577,788 filed December 22, 1995, 08/706,945 filed September 3, 1996, and 08/771,777, filed December

25 20, 1996, hereby incorporated by reference; and PCT Application No. WO96/26271). OPG dramatically increased the bone density in transgenic mice expressing the OPG polypeptide and reduced the extent of bone loss when administered to ovariectomized rats. An analysis of OPG

30 activity in in vitro osteoclast formation revealed that OPG does not interfere with the growth and differentiation of monocyte/macrophage precursors, but more likely blocks the differentiation of osteoclasts from monocyte/macrophage precursors. Thus OPG appears

to have specificity in regulating the extent of osteoclast formation.

OPG comprises two polypeptide domains having different structural and functional properties. The amino-terminal domain spanning about residues 22-194 of the full-length polypeptide (the N-terminal methionine is designated residue 1) shows homology to other members of the tumor necrosis factor receptor (TNFR) family, especially TNFR-2, through conservation of cysteine rich domains characteristic of TNFR family members. The carboxy terminal domain spanning residues 194-401 has no significant homology to any known sequences. Unlike a number of other TNFR family members, OPG appears to be exclusively a secreted protein and does not appear to be synthesized as a membrane associated form.

Based upon its activity as a negative regulator of osteoclast formation, it is postulated that OPG may bind to a polypeptide factor involved in osteoclast differentiation and thereby block one or more terminal steps leading to formation of a mature osteoclast.

It is therefore an object of the invention to identify polypeptides which interact with OPG. Said polypeptides may play a role in osteoclast maturation and may be useful in the treatment of bone diseases.

Summary of the Invention

A novel member of the tumor necrosis factor family has been identified from a murine cDNA library expressed in COS cells screened using a recombinant OPG-Fc fusion protein as an affinity probe. The new polypeptide is a transmembrane OPG binding protein which is predicted to be 316 amino acids in length, and has an amino terminal cytoplasmic domain, a transmembrane domain, and a carboxy terminal extracellular domain. OPG

binding proteins of the invention may be membrane-associated or may be in soluble form.

The invention provides for nucleic acids encoding an OPG binding protein, vectors and host cells
5 expressing the polypeptide, and method for producing recombinant OPG binding protein. Antibodies or fragments thereof which specifically bind OPG binding protein are also provided.

OPG binding proteins may be used in assays to
10 quantitate OPG levels in biological samples, identify cells and tissues that display OPG binding protein, and identify new OPG and OPG binding protein family members. Methods of identifying compounds which interact with OPG binding protein are also provided. Such compounds
15 include nucleic acids, peptides, proteins, carbohydrates, lipids or small molecular weight organic molecules and may act either as agonists or antagonists of OPG binding protein activity.

OPG binding proteins are involved in
20 osteoclast differentiation and the level of osteoclast activity in turn modulates bone resorption. OPG binding protein agonists and antagonists modulate osteoclast formation and bone resorption and may be used to treat bone diseases characterized by changes in bone
25 resorption, such as osteoporosis, hypercalcemia, bone loss due to arthritis metastasis, immobilization or periodontal disease, Paget's disease, osteopetrosis, prosthetic loosening and the like. Pharmaceutical compositions comprising OPG binding proteins and OPG
30 binding protein agonists and antagonists are also encompassed by the invention.

Description of the Figures

35 Figure 1. Structure and sequence of the 32D-F3 insert encoding OPG binding protein. Predicted

transmembrane domain and sites for asparagine-linked carbohydrate chains are underlined.

Figure 2. OPG binding protein expression in
5 COS-7 cells transfected with pcDNA/32D-F3. Cells were
lipofected with pcDNA/32D-F3 DNA, the assayed for
binding to either goat anti-human IgG1 alkaline
phosphatase conjugate (secondary alone), human
OPG[22-201]-Fc plus secondary (OPG-Fc), or a chimeric
10 ATAR extracellular domain-Fc fusion protein (sATAR-Fc).
ATAR is a new member of the TNFR superfamily, and the
sATAR-Fc fusion protein serves as a control for both
human IgG1 Fc domain binding, and generic TNFR related
protein, binding to 32D cell surface molecules.

15
Figure 3. Expression of OPG binding protein
in human tissues. Northern blot analysis of human
tissue mRNA (Clontech) using a radiolabeled 32D-F3
derived hybridization probe. Relative molecular mass is
20 indicated at the left in kilobase pairs (kb). Arrowhead
on right side indicates the migration of an
approximately 2.5 kb transcript detected in lymph node
mRNA. A very faint band of the same mass is also
detected in fetal liver.

25
Figure 4. Structure and sequence of the
pcDNA/ hu OPGbp 1.1 insert encoding the human OPG
binding protein. The predicted transmembrane domain and
site for asparagine-linked carbohydrate chains are
30 underlined.

Figure 5. Stimulation of osteoclast
development in vitro from bone marrow macrophage and ST2
cell cocultures treated with recombinant murine OPG
35 binding protein [158-316]. Cultures were treated with
varying concentrations of murine OPG binding protein

ranging from 1.6 to 500 ng/ml. After 8-10 days, cultures were lysed, and TRAP activity was measured by solution assay. In addition, some cultures were simultaneously treated with 1, 10, 100, 500, and 1000
5 ng/ml of recombinant murine OPG [22-401]-Fc protein. Murine OPG binding protein induces a dose-dependent stimulation in osteoclast formation, whereas OPG [22-401]-Fc inhibits osteoclast formation.

10 Figure 6. Stimulation of osteoclast development from bone marrow precursors in vitro in the presence of M-CSF and murine OPG binding protein [158-316]. Mouse bone marrow was harvested, and cultured in the presence 250, 500, 1000, and 2000 U/ml of M-CSF.
15 Varying concentrations of OPG binding protein [158-316], ranging from 1.6 to 500 ng/ml, were added to these same cultures. Osteoclast development was measured by TRAP solution assay.

20 Figure 7. Osteoclasts derived from bone marrow cells in the presence of both M-CSF and OPG binding protein [158-316] resorb bone in vitro. Bone marrow cells treated with either M-CSF, OPG binding protein, or with both factors combined, were plated onto
25 bone slices in culture wells, and were allowed to develop into mature osteoclasts. The resulting cultures were then stained with Toluidine Blue (left column), or histochemically to detect TRAP enzyme activity (right column). In cultures receiving both factors, mature
30 osteoclasts were formed that were capable of eroding bone as judged by the presence of blue stained pits on the bone surface. This correlated with the presence of multiple large, multinucleated, TRAP positive cells.

35 Figure 8. Graph showing the whole blood ionized calcium (iCa) levels from mice injected with OPG

binding protein, 51 hours after the first injection, and in mice also receiving concurrent OPG administration. OPG binding protein significantly and dose dependently increased iCa levels. OPG (1mg/kg/day) completely
5 blocked the increase in iCa at a dose of OPG binding protein of 5ug/day, and partially blocked the increase at a dose of OPG binding protein of 25ug/day. (*), different to vehicle treated control ($p < 0.05$). (#), OPG treated iCa level significantly different to level
10 in mice receiving that dose of OPG binding protein alone ($p < 0.05$).

Figure 9. Radiographs of the left femur and tibia in mice treated with 0, 5, 25 or 100ug/day of OPG
15 binding protein for 3.5 days. There is a dose dependent decrease in bone density evident most clearly in the proximal tibial metaphysis of these mice, and that is profound at a dose of 100ug/day.

20 Detailed Description of the Invention

The invention provides for a polypeptide referred to as an OPG binding protein, which specifically binds OPG and is involved in osteoclast differentiation. A cDNA clone encoding the murine form
25 of the polypeptide was identified from a library prepared from a mouse myelomonocytic cell line 32-D and transfected into COS cells. Transfectants were screened for their ability to bind to an OPG[22-201]-Fc fusion polypeptide (Example 1). The nucleic acid sequence
30 revealed that OPG binding protein is a novel member of the TNF family and is most closely related to AGP-1, a polypeptide previously described in co-owned and co-pending U.S. Serial No. 08/660,562, filed June 7, 1996. (A polypeptide identical to AGP-1 and designated TRAIL
35 is described in Wiley et al. Immunity 3, 673-682

(1995)). OPG binding protein is predicted to be a type II transmembrane protein having a cytoplasmic domain at the amino terminus, a transmembrane domain, and a carboxy terminal extracellular domain (Figure 1). The amino terminal cytoplasmic domain spans about residues 1-48, the transmembrane domain spans about residues 49-69 and the extracellular domain spans about residues 70-316 as shown in Figure 1 (SEQ ID NO:___). The membrane-associated protein specifically binds OPG (Figure 2). Thus OPG binding protein and OPG share many characteristics of a receptor-ligand pair although it is possible that other naturally-occurring receptors for OPG binding protein exist.

A DNA clone encoding human OPG binding protein was isolated from a lymph node cDNA library. The human sequence (Figure 4) is homologous to the murine sequence. Purified soluble murine OPG binding protein stimulated osteoclast formation in vitro and induced hypercalcemia and bone resorption in vivo.

OPG binding protein refers to a polypeptide having an amino acid sequence of mammalian OPG binding protein, or a fragment, analog, or derivative thereof, and having at least the activity of binding OPG. In preferred embodiments, OPG binding protein is of murine or human origin. In another embodiment, OPG binding protein is a soluble protein having, in one form, an isolated extracellular domain separate from cytoplasmic and transmembrane domains. OPG binding protein is involved in osteoclast differentiation and in the rate and extent of bone resorption, and was found to stimulate osteoclast formation and stimulate bone resorption.

Nucleic Acids

The invention provides for isolated nucleic acids encoding OPG binding proteins. As used herein, the term nucleic acid comprises cDNA, genomic DNA, wholly or partially synthetic DNA, and RNA. The nucleic acids of the invention are selected from the group consisting of:

- a) the nucleic acids as shown in Figure 1 (SEQ ID NO: ____) and Figure 4 (SEQ ID NO: ____);
- b) nucleic acids which hybridize to the polypeptide coding regions of the nucleic acids shown in Figure 1 (SEQ ID NO: ____) and Figure 4 (SEQ ID NO: ____); and remain hybridized to the nucleic acids under high stringency conditions; and
- c) nucleic acids which are degenerate to the nucleic acids of (a) or (b).

Nucleic acid hybridizations typically involve a multi-step process comprising a first hybridization step to form nucleic acid duplexes from single strands followed by a second hybridization step carried out under more stringent conditions to selectively retain nucleic acid duplexes having the desired homology. The conditions of the first hybridization step are generally not crucial, provided they are not of higher stringency than the second hybridization step. Generally, the second hybridization is carried out under conditions of high stringency, wherein "high stringency" conditions refers to conditions of temperature and salt which are about 12-20°C below the melting temperature (T_m) of a perfect hybrid of part or all of the complementary strands corresponding to Figure 1 (SEQ. ID. NO: ____) and Figure 4 (SEQ ID NO: ____). In one embodiment, "high stringency" conditions refer to conditions of about 65°C and not more than about 1M Na+. It is understood that

salt concentration, temperature and/or length of incubation may be varied in either the first or second hybridization steps such that one obtains the hybridizing nucleic acid molecules according to the invention. Conditions for hybridization of nucleic acids and calculations of T_m for nucleic acid hybrids are described in Sambrook et al. Molecular Cloning: A Laboratory Manual Cold Spring Harbor Laboratory Press, New York (1989).

The nucleic acids of the invention may hybridize to part or all of the polypeptide coding regions of OPG binding protein as shown in Figure 1 (SEQ ID NO: ____) and Figure 4 (SEQ ID NO: ____); and therefore may be truncations or extensions of the nucleic acid sequences shown therein. Truncated or extended nucleic acids are encompassed by the invention provided that they retain at least the property of binding OPG. In one embodiment, the nucleic acid will encode a polypeptide of at least about 10 amino acids. In another embodiment, the nucleic acid will encode a polypeptide of at least about 20 amino acids. In yet another embodiment, the nucleic acid will encode a polypeptide of at least about 50 amino acids. The hybridizing nucleic acids may also include noncoding sequences located 5' and/or 3' to the OPG binding protein coding regions. Noncoding sequences include regulatory regions involved in expression of OPG binding protein, such as promoters, enhancer regions, translational initiation sites, transcription termination sites and the like.

In preferred embodiments, the nucleic acids of the invention encode mouse or human OPG binding protein. Nucleic acids may encode a membrane bound form of OPG binding protein or soluble forms which lack a functional transmembrane region. The predicted transmembrane

region for murine OPG binding protein includes amino acid residues 49-69 inclusive as shown in Figure 1 (SEQ. ID. NO: ____). The predicted transmembrane region for human OPG binding protein includes residues 49-69 as
5 shown in Figure 4 (SEQ ID NO:____). Substitutions which replace hydrophobic amino acid residues in this region with neutral or hydrophilic amino acid residues would be expected to disrupt membrane association and result in soluble OPG binding protein. In addition, deletions of
10 part or all the transmembrane region would also be expected to produce soluble forms of OPG binding protein. Nucleic acids encoding amino acid residues 70-316 as shown in Figure 1 (SEQ ID NO:____), or fragments and analogs thereof, encompass soluble OPG
15 binding proteins.

Nucleic acids encoding truncated forms of soluble human OPG binding proteins are also included. Soluble forms include residues 69-317 as shown in Figure 4 (SEQ ID NO: ____) and truncations thereof. In one
20 embodiment, N-terminal truncations generate polypeptides from residues, 70-317, 71-317, 72-317, and so forth. In another embodiment, nucleic acids encode soluble OPGbp comprising residues 69-317 and N-terminal truncations thereof up to OPGbp [158-317], or alternatively, up to
25 OPGbp [166-317].

Plasmid phuOPGbp 1.1 in E. coli strain DH10 encoding human OPG binding protein was deposited with the American Type Culture Collection, Rockville, MD on June 13, 1997.

30 Nucleic acid sequences of the invention may be used for the detection of sequences encoding OPG binding protein in biological samples. In particular, the sequences may be used to screen cDNA and genomic libraries for related OPG binding protein sequences,
35 especially those from other species. The nucleic acids are also useful for modulating levels of OPG binding

protein by anti-sense technology or in vivo gene
expression. Development of transgenic animals
expressing OPG binding protein is useful for production
of the polypeptide and for the study of in vivo
5 biological activity.

Vectors and Host Cells

The nucleic acids of the invention will be
linked with DNA sequences so as to express biologically
10 active OPG binding protein. Sequences required for
expression are known to those skilled in the art and
include promoters and enhancer sequences for initiation
of RNA synthesis, transcription termination sites,
ribosome binding sites for the initiation of protein
15 synthesis, and leader sequences for secretion.
Sequences directing expression and secretion of OPG
binding protein may be homologous, i.e., the sequences
are identical or similar to those sequences in the
genome involved in OPG binding protein expression and
20 secretion, or they may be heterologous. A variety of
plasmid vectors are available for expressing OPG binding
protein in host cells (see, for example, Methods in
Enzymology v. 185, Goeddel, D.V. ed., Academic Press
(1990)). For expression in mammalian host cells, a
25 preferred embodiment is plasmid pDSR α described in
PCT Application No. 90/14363. For expression in
bacterial host cells, preferred embodiments include
plasmids harboring the lux promoter (see co-owned and
co-pending U.S. Serial No. 08/577,778, filed December
30 22, 1995). In addition, vectors are available for the
tissue-specific expression of OPG binding protein in
transgenic animals. Retroviral and adenovirus-based
gene transfer vectors may also be used for the
expression of OPG binding protein in human cells for in
35 vivo therapy (see PCT Application No. 86/00922).

Procaryotic and eucaryotic host cells expressing OPG binding protein are also provided by the invention. Host cells include bacterial, yeast, plant, insect or mammalian cells. OPG binding protein may also
5 be produced in transgenic animals such as mice or goats. Plasmids and vectors containing the nucleic acids of the invention are introduced into appropriate host cells using transfection or transformation techniques known to one skilled in the art. Host cells may contain DNA
10 sequences encoding OPG binding protein as shown in Figure 1 or a portion thereof, such as the extracellular domain or the cytoplasmic domain. Nucleic acids encoding OPG binding proteins may be modified by substitution of codons which allow for optimal
15 expression in a given host. At least some of the codons may be so-called preference codons which do not alter the amino acid sequence and are frequently found in genes that are highly expressed. However, it is understood that codon alterations to optimize expression
20 are not restricted to the introduction of preference codons. Examples of preferred mammalian host cells for OPG binding protein expression include, but are not limited to COS, CHO^d-, 293 and 3T3 cells. A preferred bacterial host cell is Escherichia coli.

25

Polypeptides

The invention also provides OPG binding protein as the product of procaryotic or eucaryotic expression of an exogenous DNA sequence, i.e., OPG
30 binding protein is recombinant OPG binding protein. Exogenous DNA sequences include cDNA, genomic DNA and synthetic DNA sequences. OPG binding protein may be the product of bacterial, yeast, plant, insect or mammalian cells expression, or from cell-free translation systems.
35 OPG binding protein produced in bacterial cells will

have an N-terminal methionine residue. The invention also provides for a process of producing OPG binding protein comprising growing procaryotic or eucaryotic host cells transformed or transfected with nucleic acids encoding OPG binding protein and isolating polypeptide expression products of the nucleic acids.

Polypeptides which are mamalian OPG binding proteins or are fragments, analogs or derivatives thereof are encompassed by the invention. In a preferred embodiment, the OPG binding protein is human OPG binding protein. A fragment of OPG binding protein refers to a polypeptide having a deletion of one or more amino acids such that the resulting polypeptide has at least the property of binding OPG. Said fragments will have deletions originating from the amino terminal end, the carboxy terminal end, and internal regions of the polypeptide. Fragments of OPG binding protein are at least about ten amino acids, at least about 20 amino acids, or at least about 50 amino acids in length. In preferred embodiments, OPG binding protein will have a deletion of one or more amino acids from the transmembrane region (amino acid residues 49-69 as shown in Figure 1), or, alternatively, one or more amino acids from the amino-terminus up to and/or including the transmembrane region (amino acid residues 1-49 as shown in Figure 1). In another embodiment, OPG binding protein is a soluble protein comprising, for example, amino acid residues 69-316, or 70-316, or N-terminal or C-terminal truncated forms thereof, which retain OPG binding activity. OPG binding protein is also a human soluble protein as shown in Figure 4 comprising residues 69-317 as shown in Figure 4 and N-terminal truncated forms thereof, e.g., 70-517, 71-517, 71-317, 72-317 and so forth. In a preferred embodiment, the soluble human OPG binding protein comprising residues 69-317 and

N-terminal truncation thereof up to OPGbp [158-317], or alternatively up to OPG [166-317].

5 An analog of an OPG binding protein refers to a polypeptide having a substitution or addition of one or more amino acids such that the resulting polypeptide has at least the property of binding OPG. Said analogs will have substitutions or additions at any place along the polypeptide. Preferred analogs include those of soluble OPG binding proteins. Fragments or analogs may
10 be naturally occurring, such as a polypeptide product of an allelic variant or a mRNA splice variant, or they may be constructed using techniques available to one skilled in the art for manipulating and synthesizing nucleic acids. The polypeptides may or may not have an amino
15 terminal methionine residue

Also included in the invention are derivatives of OPG binding protein which are polypeptides that have undergone post-translational modifications (e.g., addition of N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment
20 of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition of an N-terminal methionine residue as a result of procaryotic host cell expression. In particular, chemically modified
25 derivatives of OPG binding protein which provide additional advantages such as increased stability, longer circulating time, or decreased immunogenicity are contemplated. Of particular use is modification with
30 water soluble polymers, such as polyethylene glycol and derivatives thereof (see for example U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene
35 glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and

the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties. Polypeptides
5 may also be modified at pre-determined positions in the polypeptide, such as at the amino terminus, or at a selected lysine or arginine residue within the polypeptide. Other chemical modifications provided include a detectable label, such as an enzymatic,
10 fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

OPG binding protein chimeras comprising part or all of an OPG binding protein amino acid sequence fused to a heterologous amino acid sequence are also
15 included. The heterologous sequence may be any sequence which allows the resulting fusion protein to retain the at least the activity of binding OPG. In a preferred embodiment, the carboxy terminal extracellular domain of OPG binding protein is fused to a heterologous sequence.
20 Such sequences include heterologous cytoplasmic domains that allow for alternative intracellular signalling events, sequences which promote oligomerization such as the Fc region of IgG, enzyme sequences which provide a label for the polypeptide, and sequences which provide
25 affinity probes, such as an antigen-antibody recognition.

The polypeptides of the invention are isolated and purified from tissues and cell lines which express OPG binding protein, either extracted from lysates or
30 from conditioned growth medium, and from transformed host cells expressing OPG binding protein. OPG binding protein may be obtained from murine myelomonocytic cell line 32-D (ATCC accession no. CRL-11346). Human OPG binding protein, or nucleic acids encoding same, may be
35 isolated from human lymph node or fetal liver tissue.

Isolated OPG binding protein is free from association with human proteins and other cell constituents.

A method for the purification of OPG binding protein from natural sources (e.g. tissues and cell
5 lines which normally express OPG binding protein) and from transfected host cells is also encompassed by the invention. The purification process may employ one or more standard protein purification steps in an appropriate order to obtain purified protein. The
10 chromatography steps can include ion exchange, gel filtration, hydrophobic interaction, reverse phase, chromatofocusing, affinity chromatography employing an anti-OPG binding protein antibody or biotin-streptavidin affinity complex and the like.

15

Antibodies

Antibodies specifically binding the polypeptides of the invention are also encompassed by the invention. The antibodies may be produced by
20 immunization with full-length OPG binding protein, soluble forms of OPG binding protein, or a fragment thereof. The antibodies of the invention may be polyclonal or monoclonal, or may be recombinant antibodies, such as chimeric antibodies wherein the
25 murine constant regions on light and heavy chains are replaced by human sequences, or CDR-grafted antibodies wherein only the complementary determining regions are of murine origin. Antibodies of the invention may also be human antibodies prepared, for example, by
30 immunization of transgenic animals capable of producing human antibodies (see, for example, PCT Application No. WO93/12227). The antibodies are useful for detecting OPG binding protein in biological samples, thereby allowing the identification of cells or tissues
35 which produce the protein. In addition, antibodies which bind to OPG binding protein and block interaction with

other binding compounds may have therapeutic use in modulating osteoclast differentiation and bone resorption.

Antibodies to the OPG binding protein may be
5 useful in treatment of bone diseases such as,
osteoporosis and Paget's disease. Antibodies can be
tested for binding to the OPG binding protein in the
absence or presence of OPG and examined for their
ability to inhibit ligand (OPG binding protein) mediated
10 osteoclastogenesis and/or bone resorption. It is also
anticipated that the peptides themselves may act as an
antagonist of the ligand:receptor interaction and
inhibit ligand-mediated osteoclastogenesis, and peptides
of the OPG binding protein will be explored for this
15 purpose as well.

Compositions

The invention also provides for pharmaceutical
20 compositions comprising a therapeutically effective
amount of the OPG binding protein of the invention
together with a pharmaceutically acceptable diluent,
carrier, solubilizer, emulsifier, preservative and/or
adjuvant. The invention also provides for
25 pharmaceutical compositions comprising a therapeutically
effective amount of an OPG binding protein agonist or
antagonist. The term "therapeutically effective amount"
means an amount which provides a therapeutic effect for
a specified condition and route of administration. The
30 composition may be in a liquid or lyophilized form and
comprises a diluent (Tris, acetate or phosphate buffers)
having various pH values and ionic strengths,
solubilizer such as Tween or Polysorbate, carriers such
as human serum albumin or gelatin, preservatives such as
35 thimerosal or benzyl alcohol, and antioxidants such as

ascrobic acid or sodium metabisulfite. Selection of a particular composition will depend upon a number of factors, including the condition being treated, the route of administration and the pharmacokinetic parameters desired. A more extensive survey of component suitable for pharmaceutical compositions is found in Remington's Pharmaceutical Sciences, 18th ed. A.R. Gennaro, ed. Mack, Easton, PA (1980).

In a preferred embodiment, compositions comprising soluble OPG binding proteins are also provided. Also encompassed are compositions comprising soluble OPG binding protein modified with water soluble polymers to increase solubility, stability, plasma half-life and bioavailability. Compositions may also comprise incorporation of soluble OPG binding protein into liposomes, microemulsions, micelles or vesicles for controlled delivery over an extended period of time. Soluble OPG binding protein may be formulated into microparticles suitable for pulmonary administration.

Compositions of the invention may be administered by injection, either subcutaneous, intravenous or intramuscular, or by oral, nasal, pulmonary or rectal administration. The route of administration eventually chosen will depend upon a number of factors and may be ascertained by one skilled in the art.

The invention also provides for pharmaceutical compositions comprising a therapeutically effective amount of the nucleic acids of the invention together with a pharmaceutically acceptable adjuvant. Nucleic acid compositions will be suitable for the delivery of part or all of the coding region of OPG binding protein and/or flanking regions to cells and tissues as part of an anti-sense therapy regimen.

Methods of Use

OPG binding proteins may be used in a variety of assays for detecting OPG and characterizing interactions with OPG. In general, the assay comprises
5 incubating OPG binding protein with a biological sample containing OPG under conditions which permit binding to OPG to OPG binding protein, and measuring the extent of binding. OPG may be purified or present in mixtures, such as in body fluids or culture medium. Assays may be
10 developed which are qualitative or quantitative, with the latter being useful for determining the binding parameters (affinity constants and kinetics) of OPG to OPG binding protein and for quantitating levels of biologically active OPG in mixtures. Assays may also be
15 used to evaluate the binding of OPG to fragments, analogs and derivatives of OPG binding protein and to identify new OPG and OPG binding protein family members.

Binding of OPG to OPG binding protein may be carried out in several formats, including cell-based
20 binding assays, membrane binding assays, solution-phase assays and immunoassays. In general, trace levels of labeled OPG are incubated with OPG binding protein samples for a specified period of time followed by measurement of bound OPG by filtration,
25 electrochemiluminescent (ECL, ORIGEN system by IGEN), cell-based or immunoassays. Homogeneous assay technologies for radioactivity (SPA; Amersham) and time resolved fluorescence (HTRF, Packard) can also be implemented. Binding is detected by labeling OPG or an
30 anti-OPG antibody with radioactive isotopes (^{125}I , ^{35}S , ^3H), fluorescent dyes (fluorescein), lanthanide (Eu^{3+}) chelates or cryptates, orbipyridyl-ruthenium (Ru^{2+}) complexes. It is understood that the choice of a labeled probe will depend upon the detection system
35 used. Alternatively, OPG may be modified with an

unlabeled epitope tag (e.g., biotin, peptides, His₆, myc) and bound to proteins such as streptavidin, anti-peptide or anti-protein antibodies which have a detectable label as described above.

5 In an alternative method, OPG binding protein may be assayed directly using polyclonal or monoclonal antibodies to OPG binding proteins in an immunoassay. Additional forms of OPG binding proteins containing epitope tags as described above may be used in solution
10 and immunoassays.

Methods for indentifying compounds which interact with OPG binding protein are also encompassed by the invention. The method comprises incubating OPG binding protein with a compound under conditions which
15 permit binding of the compound to OPG binding protein, and measuring the extent of binding. The compound may be substantially purified or present in a crude mixture. Binding compounds may be nucleic acids, proteins, peptides, carbohydrates, lipids or small molecular
20 weight organic compounds. The compounds may be further characterized by their ability to increase or decrease OPG binding protein activity in order to determine whether they act as an agonist or an antagonist.

OPG binding proteins are also useful for
25 identification of intracellular proteins which interact with the cytoplasmic domain by a yeast two-hybrid screening process. As an example, hybrid constructs comprising DNA encoding the N-terminal 50 amino acids of an OPG binding protein fused to a yeast GAL4-DNA binding
30 domain may be used as a two-hybrid bait plasmid. Positive clones emerging from the screening may be characterized further to identify interacting proteins. This information may help elucidate a intracellular signaling mechanism associated with OPG binding protein

and provide intracellular targets for new drugs that modulate bone resorption.

OPG binding protein may be used to treat conditions characterized by excessive bone density. The most common condition is osteopetrosis in which a genetic defect results in elevated bone mass and is usually fatal in the first few years of life. Osteopetrosis is preferably treated by administration of soluble OPG binding protein.

The invention also encompasses modulators (agonists and antagonists) of OPG binding protein and the methods for obtaining them. An OPG binding protein modulator may either increase or decrease at least one activity associated with OPG binding protein, such as ability to bind OPG or some other interacting molecule or to regulate osteoclast maturation. Typically, an agonist or antagonist may be a co-factor, such as a protein, peptide, carbohydrate, lipid or small molecular weight molecule, which interacts with OPG binding protein to regulate its activity. Potential polypeptide antagonists include antibodies which react with either soluble or membrane-associated forms of OPG binding protein, and soluble forms of OPG binding protein which comprise part or all of the extracellular domain of OPG binding protein. Molecules which regulate OPG binding protein expression typically include nucleic acids which are complementary to nucleic acids encoding OPG binding protein and which act as anti-sense regulators of expression.

OPG binding protein is involved in controlling formation of mature osteoclasts, the primary cell type implicated in bone resorption. An increase in the rate of bone resorption (over that of bone formation) can lead to various bone disorders collectively referred to as osteopenias, and include osteoporosis, osteomyelitis, hypercalcemia, osteopenia brought on by surgery or

steroid administration, Paget's disease, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, immobilization, prosthetic loosening and osteolytic metastasis. Conversely, a decrease in the rate of bone resorption can lead to osteopetrosis, a condition marked by excessive bone density. Agonists and antagonists of OPG binding protein modulate osteoclast formation and may be administered to patients suffering from bone disorders. Agonists and antagonists of OPG binding protein used for the treatment of osteopenias may be administered alone or in combination with a therapeutically effective amount of a bone growth promoting agent including bone morphogenic factors designated BMP-1 to BMP-12, transforming growth factor- β and TGF- β family members, fibroblast growth factors FGF-1 to FGF-10, interleukin-1 inhibitors, TNF α inhibitors, parathyroid hormone, E series prostaglandins, bisphosphonates and bone-enhancing minerals such as fluoride and calcium. Antagonists of OPG binding proteins may be particularly useful in the treatment of osteopenia.

The following examples are offered to more fully illustrate the invention, but are not construed as limiting the scope thereof.

Example 1

Identification of a cell line source for an OPG binding protein

Osteoprotegerin (OPG) negatively regulates osteoclastogenesis in vitro and in vivo. Since OPG is a TNFR-related protein, it is likely to interact with a TNF-related family member while mediating its effects. With one exception, all known members of the TNF

superfamily are type II transmembrane proteins expressed on the cell surface. To identify a source of an OPG binding protein, recombinant OPG-Fc fusion proteins were used as immunoprobes to screen for OPG binding proteins located on the surface of various cell lines and primary hematopoietic cells.

Cell lines that grew as adherent cultures in vitro were treated using the following methods: Cells were plated into 24 well tissue culture plates (Falcon), then allowed to grow to approximately 80% confluency. The growth media was then removed, and the adherent cultures were washed with phosphate buffered saline (PBS) (Gibco) containing 1% fetal calf serum (FCS). Recombinant mouse OPG [22-194]-Fc and human OPG [22-201]-Fc fusion proteins (see U.S. Serial No. 08/706,945 filed September 3, 1996) were individually diluted to 5 ug/ml in PBS containing 1% FCS, then added to the cultures and allowed to incubate for 45 min at 0°C. The OPG-Fc fusion protein solution was discarded, and the cells were washed in PBS-FCS solution as described above. The cultures were then exposed to phycoerythrin-conjugated goat F(ab') anti-human IgG secondary antibody (Southern Biotechnology Associates Cat. # 2043-09) diluted into PBS-FCS. After a 30-45 min incubation at 0°C, the solution was discarded, and the cultures were washed as described above. The cells were then analysed by immunofluorescent microscopy to detect cell lines which express a cell surface OPG binding protein.

Suspension cell cultures were analysed in a similar manner with the following modifications: The diluent and wash buffer consisted of calcium- and magnesium-free phosphate buffered saline containing 1% FCS. Cells were harvested from exponentially replicating cultures in growth media, pelleted by centrifugation, then resuspended at 1×10^7 cells/ml in a

96 well microtiter tissue culture plate (Falcon). Cells were sequentially exposed to recombinant OPG-Fc fusion proteins, then secondary antibody as described above, and the cells were washed by centrifugation between each
5 step. The cells were then analysed by fluorescence activated cell sorting (FACS) using a Becton Dickinson FACscan.

Using this approach, the murine myelomonocytic cell line 32D (ATCC accession no. CRL-11346) was found
10 to express a surface molecule which could be detected with both the mouse OPG[22-194]-Fc and the human OPG[22-201]-Fc fusion proteins. Secondary antibody alone did not bind to the surface of 32D cells nor did purified human IgG1 Fc, indicating that binding of the
15 OPG-Fc fusion proteins was due to the OPG moiety. This binding could be competed in a dose dependent manner by the addition of recombinant murine or human OPG[22-401] protein. Thus the OPG region required for its biological activity is capable of specifically binding to a
20 32D-derived surface molecule.

Example 2

Expression cloning of a murine OPG binding protein

25 A cDNA library was prepared from 32D mRNA, and ligated into the mammalian expression vector pcDNA3.1(+) (Invitrogen, San Diego, CA). Exponentially growing 32D cells maintained in the presence of recombinant
30 interleukin-3 were harvested, and total cell RNA was purified by acid guanidinium thiocyanate-phenol-chloroform extraction (Chomczynski and Sacchi. Anal. Biochem. 162, 156-159, (1987)). The poly (A+) mRNA fraction was obtained from the total RNA preparation by
35 adsorption to, and elution from, Dynabeads Oligo (dT)25

(Dynal Corp) using the manufacturer's recommended procedures. A directional, oligo-dT primed cDNA library was prepared using the Superscript Plasmid System (Gibco BRL, Gaithersburg, Md) using the manufacturer's
5 recommended procedures. The resulting cDNA was digested to completion with Sal I and Not I restriction endonuclease, then fractionated by size exclusion gel chromatography. The highest molecular weight fractions were selected, and then ligated into the polyliker
10 region of the plasmid vector pcDNA3.1(+) (Invitrogen, San Diego, CA). This vector contains the CMV promoter upstream of multiple cloning site, and directs high level expression in eukaryotic cells. The library was then electroporated into competent *E. coli* (ElectroMAX
15 DH10B, Gibco, NY), and titered on LB agar containing 100 ug/ml ampicillin. The library was then arrayed into segregated pools containing approximately 1000 clones/pool, and 1.0 ml cultures of each pool were grown for 16-20 hr at 37°C. Plasmid DNA from each culture was
20 prepared using the Qiagen QiaWell 96 Ultra Plasmid Kit (catalog #16191) following manufacturer's recommended procedures.

Arrayed pools of 32D cDNA expression library were individually lipofected into COS-7 cultures, then
25 assayed for the acquisition of a cell surface OPG binding protein. To do this, COS-7 cells were plated at a density of 1×10^6 per ml in six-well tissue culture plates (Costar), then cultured overnight in DMEM (Gibco) containing 10% FCS. Approximately 2 µg of plasmid DNA
30 from each pool was diluted into 0.5 ml of serum-free DMEM, then sterilized by centrifugation through a 0.2 µm Spin-X column (Costar). Simultaneously, 10 µl of Lipofectamine (Life Technologies Cat # 18324-012) was added to a separate tube containing 0.5ml of serum-free

DMEM. The DNA and Lipofectamine solutions were mixed, and allowed to incubate at RT for 30 min. The COS-7 cell cultures were then washed with serum-free DMEM, and the DNA-lipofectamine complexes were exposed to the
5 cultures for 2-5 hr at 37°C. After this period, the media was removed, and replaced with DMEM containing 10%FCS. The cells were then cultured for 48 hr at 37°C.

To detect cultures that express an OPG binding protein, the growth media was removed, and the cells
10 were washed with PBS-FCS solution. A 1.0 ml volume of PBS-FCS containing 5 µg/ml of human OPG[22-201]-Fc fusion protein was added to each well and incubated at RT for 1 hr. The cells were washed three times with PBS-FCS solution, and then fixed in PBS containing 2%
15 paraformaldehyde and 0.2% glutaraldehyde in PBS at RT for 5 min. The cultures were washed once with PBS-FCS, then incubated for 1 hr at 65°C while immersed in PBS-FCS solution. The cultures were allowed to cool, and the PBS-FCS solution was aspirated. The cultures
20 were then incubated with an alkaline-phosphatase conjugated goat anti-human IgG (Fc specific) antibody (SIGMA Product # A-9544) at Rt for 30 min, then washed three-times with 20 mM Tris-Cl (pH 7.6), and 137 mM NaCl. Immune complexes that formed during these steps
25 were detected by assaying for alkaline phosphatase activity using the Fast Red TR/AS-MX Substrate Kit (Pierce, Cat. # 34034) following the manufacturer's recommended procedures.

Using this approach, a total of approximately
30 300,000 independent 32D cDNA clones were screened, represented by 300 transfected pools of 1000 clones each. A single well was identified that contained cells which acquired the ability to be specifically decorated by the OPG-Fc fusion protein. This pool was subdivided
35 by sequential rounds of sib selection, yeilding a single

plasmid clone 32D-F3 (Figure 1). 32D-F3 plasmid DNA was then transfected into COS-7 cells, which were immunostained with either FITC-conjugated goat anti-human IgG secondary antibody alone, human
5 OPG[22-201]-Fc fusion protein plus secondary, or with ATAR-Fc fusion protein (ATAR also known as HVEM; Montgomery et al. Cell 87, 427-436 (1996)) (Figure 2). The secondary antibody alone did not bind to COS-7/32D-F3 cells, nor did the ATAR-Fc fusion protein.
10 Only the OPG Fc fusion protein bound to the COS-7/32D-F3 cells, indicating that 32D-F3 encoded an OPG binding protein displayed on the surface of expressing cells.

15 Example 3
OPG Binding Protein Sequence

The 32D-F3 clone isolated above contained an approximately 2.3 kb cDNA insert (Figure 1), which was
20 sequenced in both directions on an Applied Biosystems 373A automated DNA sequencer using primer-driven Taq dye-terminator reactions (Applied Biosystems) following the manufacturer's recommended procedures. The resulting nucleotide sequence obtained was compared to
25 the DNA sequence database using the FASTA program (GCG, Univeristy of Wisconsin), and analysed for the presence of long open reading frames (LORF's) using the "Six-way open reading frame" application (Frames) (GCG, Univeristy of Wisconsin). A LORF of 316 amino acid (aa)
30 residues beginning at methionine was detected in the appropriate orientation, and was preceded by a 5' untranslated region of about 150 bp. The 5' untranslated region contained an in-frame stop codon upstream of the predicted start codon. This indicates
35 that the structure of the 32D-F3 plasmid is consistent

with its ability to utilize the CMV promotor region to direct expression of a 316 aa gene product in mammalian cells.

The predicted OPG binding protein sequence was
5 then compared to the existing database of known protein
sequences using a modified version of the FASTA program
(Pearson, Meth. Enzymol. 183, 63-98 (1990)). The amino
acid sequence was also analysed for the presence of
specific motifs conserved in all known members of the
10 tumor necrosis factor (TNF) superfamily using the
sequence profile method of (Gribskov et al. Proc. Natl.
Acad. Sci. USA 83, 4355-4359 (1987)), as modified by
Lüethy et al. Protein Sci. 3, 139-146 (1994)). There
appeared to be significant homology throughout the OPG
15 binding protein to several members of the TNF
superfamily. The mouse OPG binding protein appear to be
most closely related to the mouse and human homologs of
both TRAIL and CD40 ligand. Further analysis of the OPG
binding protein sequence indicated a strong match to the
20 TNF superfamily, with a highly significant Z score of
19.46.

The OPG binding protein amino acid sequence
contains a probable hydrophobic transmembrane domain
that begins at a M49 and extends to L69. Based on this
25 configuration relative to the methionine start codon,
the OPG binding protein is predicted to be a type II
transmembrane protein, with a short N-terminal
intracellular domain, and a longer C-terminal
extracellular domain (Figure 4). This would be similar
30 to all known TNF family members, with the exception of
lymphotoxin alpha (Nagata and Golstein, Science 267,
1449-1456 (1995)).

Example 4

Expression of human OPG binding protein mRNA

5 Multiple human tissue northern blots
(Clontech, Palo Alto, CA) were probed with a ³²P-dCTP
labelled 32D-F3 restriction fragment to detect the size
of the human transcript and to determine patterns of
expression. Northern blots were prehybridized in 5X
10 SSPE, 50% formamide, 5X Denhardt's solution, 0.5% SDS,
and 100 µg/ml denatured salmon sperm DNA for 2-4 hr at
42°C. The blots were then hybridized in 5X SSPE, 50%
formamide, 2X Denhardt's solution, 0.1% SDS, 100 µg/ml
denatured salmon sperm DNA, and 5 ng/ml labelled probe
15 for 18-24 hr at 42°C. The blots were then washed in 2X
SSC for 10 min at RT, 1X SSC for 10 min at 50°C, then in
0.5X SSC for 10-15 min.

Using a probe derived from the mouse cDNA and
hybridization under stringent conditions, a predominant
20 mRNA species with a relative molecular mass of about 2.5
kb was detected in lymph nodes (Figure 3). A faint
signal was also detected at the same relative molecular
mass in fetal liver mRNA. No OPG binding protein
transcripts were detected in the other tissues examined.
25 The data suggest that expression of OPG binding protein
mRNA was extremely restricted in human tissues. The
data also indicate that the cDNA clone isolated is very
close to the size of the native transcript, suggesting
32D-F3 is a full length clone.

Example 5

Molecular cloning of the human OPG binding protein

5 The human homolog of the OPG binding protein
is expressed as an approximately 2.5 kb mRNA in human
peripheral lymph nodes and is detected by hybridization
with a mouse cDNA probe under stringent hybridization
conditions. DNA encoding human OPG binding protein is
10 obtained by screening a human lymph node cDNA library by
either recombinant bacteriophage plaque, or transformed
bacterial colony, hybridization methods (Sambrook et
al. Molecular Cloning: A Laboratory Manual Cold Spring
Harbor Press, New York (1989)). To this the phage or
15 plasmid cDNA library are screened using radioactively-
labeled probes derived from the murine OPG binding
protein clone 32D-F3. The probes are used to screen
nitrocellulose filter lifted from a plated library.
These filters are prehybridized and then hybridized
20 using conditions specified in Example 4, ultimately
giving rise to purified clones of the human OPG binding
protein cDNA. Inserts obtained from any human OPG
binding protein clones would be sequenced and analysed
as described in Example 3.

25 A human lymph node poly A+ RNA (Clontech,
Inc., Palo Alto, CA) was analysed for the presence of
OPG-bp transcripts as previously in U.S. Serial No.
08/577,788, filed December 22, 1995. A northern blot of
this RNA sample probed under stringent conditions with a
30 32P-labeled mouse OPG-bp probe indicated the presence of
human OPG-bp transcripts. An oligo dT-primed cDNA
library was then synthesized from the lymph node mRNA
using the SuperScript kit (GIBCO life Technologies,
Gaithersburg, MD) as described in example 2. The
35 resulting cDNA was size selected, and the high molecular

fraction ligated to plasmid vector pcDNA 3.1 (+)
(Invitrogen, San Diego, CA). Electrocompetent *E. coli*
DH10 (GIBCO life Technologies, Gaithersburg, MD) were
transformed, and 1×10^6 ampicillin resistant
5 transformants were screened by colony hybridization
using a ^{32}P -labeled mouse OPG binding protein probe.

A plasmid clone of putative human OPG binding
protein cDNA was isolated, phuOPGbp-1.1, and contained a
2.3 kp insert. The resulting nucleotide sequence of the
10 phuOPGbp-1.1 insert was approximately 80-85% homologous
to the mouse OPG binding protein cDNA sequence.
Translation of the insert DNA sequence indicated the
presence of a long open reading frame predicted to
encode a 317 aa polypeptide (Figure 4). Comparison of
15 the mouse and human OPG-bp polypeptides shows that they
are ~87% identical, indicating that this protein is
highly conserved during evolution.

The human OPG binding protein DNA and protein
sequences were not present in Genbank, and there were no
20 homologous EST sequences. As with the murine homolog,
the human OPG binding protein shows strong sequence
similarity to all members of the TNF α superfamily of
cytokines.

25

Example 6

Cloning and Bacterial Expression of OPG binding protein

PCR amplification employing the primer pairs
30 and templates described below are used to generate
various forms of murine OPG binding proteins. One
primer of each pair introduces a TAA stop codon and a
unique XhoI or SacII site following the carboxy terminus
of the gene. The other primer of each pair introduces a
35 unique NdeI site, a N-terminal methionine, and optimized

codons for the amino terminal portion of the gene. PCR and thermocycling is performed using standard recombinant DNA methodology. The PCR products are purified, restriction digested, and inserted into the unique NdeI and XhoI or SacII sites of vector pAMG21 (ATCC accession no. 98113) and transformed into the prototrophic E. coli 393 or 2596. Other commonly used E. coli expression vectors and host cells are also suitable for expression. After transformation, the clones are selected, plasmid DNA is isolated and the sequence of the OPG binding protein insert is confirmed.

pAMG21-Murine OPG binding protein [75-316]

This construct was engineered to be 242 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met(75)-Asp-Pro-Asn-Arg-----Gln-Asp-Ile-Asp(316)-COOH. The template to be used for PCR was pcDNA/32D-F3 and oligonucleotides #1581-72 and #1581-76 were the primer pair to be used for PCR and cloning this gene construct.

1581-72:

5'-GTTCTCCTCATATGGATCCAAACCGTATTTCTGAAGACAGCACTCACTGCTT-3'

(SEQ ID NO:___)

1581-76:

5'-TACGCACTCCGCGGTTAGTCTATGTCCTGAACTTTGA-3'

(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [95-316]

This construct was engineered to be 223 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met-His(95)-Glu-Asn-Ala-Gly-----Gln-Asp-Ile-Asp(316)-COOH. The template used for PCR was pcDNA/32D-F3 and oligonucleotides #1591-90 and

#1591-95 were the primer pair used for PCR and cloning this gene construct.

1591-90:

5 5'-ATTTGATTCTAGAAGGAGGAATAACATATGCATGAAAACGCAGGTCTGCAG-3'
(SEQ ID NO:___)

1591-95:

5'-TATCCGCGGATCCTCGAGTTAGTCTATGTCCTGAACTTTGAA-3'
(SEQ ID NO:___)

10

pAMG21-Murine OPG binding protein [107-316]

This construct was engineered to be 211 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met-Ser(107)-Glu-Asp-Thr-Leu----
15 ---Gln-Asp-Ile-Asp(316)-COOH. The template used for PCR was pCDNA/32D-F3 and oligonucleotides #1591-93 and #1591-95 were the primer pair used for PCR and cloning this gene construct.

20 1591-93:

5'-ATTTGATTCTAGAAGGAGGAATAACATATGTCTGAAGACACTCTGCCGGACTCC-3'
(SEQ ID NO:___)

1591-95:

25 5'-TATCCGCGGATCCTCGAGTTAGTCTATGTCCTGAACTTTGAA-3'
(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [118-316]

This construct was engineered to be 199 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met(118)-Lys-Gln-Ala-Phe-Gln----
30 ---Gln-Asp-Ile-Asp(316)-COOH. The template used for PCR was pCDNA/32D-F3 and oligonucleotides #1591-94 and #1591-95 were the primer pair used for PCR and cloning
35 this gene construct.

1591-94:

5'-ATTTGATTCTAGAAGGAGGAATAACATATGAAACAAGCTTTTCAGGGG-3'

(SEQ ID NO:___)

1591-95:

5 5'-TATCCGCGGATCCTCGAGTTAGTCTATGTCCTGAACTTTGAA-3'

(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [128-316]

10 This construct was engineered to be 190 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met-Lys(128)-Glu-Leu-Gln-His-----Gln-Asp-Ile-Asp(316)-COOH. The template used for PCR was pcDNA/32D-F3 and oligonucleotides #1591-91 and #1591-95 were the primer pair used for PCR and cloning
15 this gene construct.

1591-91:

5'-ATTTGATTCTAGAAGGAGGAATAACATATGAAAGAACTGCAGCACATTGTG-3'

(SEQ ID NO:___)

20 1591-95:

5'-TATCCGCGGATCCTCGAGTTAGTCTATGTCCTGAACTTTGAA-3'

(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [137-316]

25 This construct was engineered to be 181 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met-Gln(137)-Arg-Phe-Ser-Gly-----Gln-Asp-Ile-Asp(316)-COOH. The template used for PCR was pcDNA/32D-F3 and oligonucleotides #1591-92 and
30 #1591-95 were the primer pair used for PCR and cloning this gene construct.

1591-92:

5'-ATTTGATTCTAGAAAGGAGGAATAACATATGCAGCGTTTCTCTGGTGCTCCA-3'

(SEQ ID NO:___)

5 1591-95:

5'-TATCCGCGGATCCTCGAGTTAGTCTATGTCCTGAACTTTGAA-3'

(SEQ ID NO:___)

10 pAMG21-Murine OPG binding protein [146-316]

This construct is engineered to be 171 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met(146)-Glu-Gly-Ser-Trp-----Gln-Asp-Ile-Asp(316)-COOH. The template to be used for PCR is pAMG21-murine OPG binding protein [75-316] described above and oligonucleotides #1600-98 and #1581-76 will be the primer pair to be used for PCR and cloning this gene construct.

20 1600-98:

5'- GTTCTCCTCATATGGAAGGTTCTTGGTTGGATGTGGCCCA-3'

(SEQ ID NO:___)

1581-76:

5'-TACGCAC'TCCGCGGTTAGTCTATGTCCTGAACTTTGA-3'

25 (SEQ ID NO:___)

pAMG21-Murine OPG binding protein [156-316]

This construct is engineered to be 162 amino acids in length and have the following N-terminal and C-terminal residues, NH₂-Met-Arg(156)-Gly-Lys-Pro-----Gln-Asp-Ile-Asp(316)-COOH. The template to be used for PCR is pAMG21-murine OPG binding protein [158-316] below and oligonucleotides #1619-86 and #1581-76 will be the primer pair to be used for PCR and cloning this gene construct.

1619-86:

5'- GTTCTCCTCATATGCGTGGTAAACCTGAAGCTCAACCATTGCA-3'
(SEQ ID NO:___)

1581-76:

5 5'-TACGCACTCCGCGGTTAGTCTATGTCCTGAACTTTGA-3'
(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [158-316]

This construct was engineered to be 160 amino
10 acids in length and have the following N-terminal and
C-terminal residues, NH₂-Met-Lys(158)-Pro-Glu-Ala-----
Gln-Asp-Ile-Asp(316)- COOH. The template to be used for
PCR was pCDNA/32D-F3 and oligonucleotides #1581-73 and
#1581-76 were the primer pair to be used for PCR and
15 cloning this gene construct.

1581-73:

5'-GTTCTCCTCATATGAAACCTGAAGCTCAACCATTGTCACACCTCACCATCAAT-3'
(SEQ ID NO:___)

20 1581-76:

5'-TACGCACTCCGCGGTTAGTCTATGTCCTGAACTTTGA-3'
(SEQ ID NO:___)

pAMG21-Murine OPG binding protein [166-316]

This construct is engineered to be 152 amino
25 acids in length and have the following N-terminal and
C-terminal residues, NH₂-Met-His(166)-Leu-Thr-Ile-----
Gln-Asp-Ile-Asp(316)- COOH. The template to be used for
PCR is pCDNA/32D-F3 and oligonucleotides #1581-75 and
30 #1581-76 will be the primer pair to be used for PCR and
cloning this gene construct.

1581-75:

5'-GTTCTCCTCATATGCATTTAACTATTAACGCTGCATCTATCCCAT

CGGGTTCCTAATAAGTCACT-3' (SEQ ID NO:___)

5 1581-76:

5'-TACGCACTCCGCGGTTAGTCTATGTCTGAACTTTGA-3' (SEQ ID NO:___)

pAMG21-Murine OPG binding protein [168-316]

This construct is engineered to be 150 amino
10 acids in length and have the following N-terminal and
C-terminal residues, NH₂-Met-Thr(168)-Ile-Asn-Ala-----
Gln-Asp-Ile-Asp(316)-COOH. The template to be used for
PCR is pcDNA/32D-F3 and oligonucleotides #1581-74 and
#1581-76 will be the primer pair to be used for PCR and
15 cloning.

1581-74:

5'-GTTCTCCTCATATGACTATTAACGCTGCATCTATCCCATCGGGTTCCTAATAAGTCACT-3'

(SEQ ID NO:___)

20 1581-76:

5'-TACGCACTCCGCGGTTAGTCTATGTCTGAACTTTGA-3' (SEQ ID NO:___)

It is understood that the above constructs are examples
and one skilled in the art may readily obtain other
25 forms of OPG binding protein using the general
methodology presented her.

Recombinant bacterial constructs pAMG21-murine
OPG binding protein [75-316], [95-316], [107-316], [118-
316], [128-316], [137-316], and [158-316] have been
30 cloned, DNA sequence confirmed, and levels of
recombinant gene product expression following induction
has been examined. All constructs produced levels of
recombinant gene product which was readily visible
following SDS polyacrylamide gel electrophoresis and
35 coomassie staining of crude lysates. Growth of
transformed E. coli 393 or 2596, induction of OPG

binding protein expression and isolation of inclusion bodies containing OPG binding protein is done according to procedures described in U.S. Serial No. 08/577,788 filed December 22, 1995. Purification of OPG binding proteins from inclusion bodies requires solubilization and renaturing of OPG binding protein using procedures available to one skilled in the art. Recombinant murine OPG binding protein [158-316] was found to be produced mostly insolubly, but about 40% was found in the soluble fraction. Recombinant protein was purified from the soluble fraction as described below and its bioactivity examined.

Example 7

Purification of recombinant murine OPG ligand [158-316]

Frozen bacterial cells harboring expressed murine OPG binding protein (158-316) were thawed and resuspended in 20mM tris-HCl pH 7.0, 10mM EDTA. The cell suspension (20%w/v) was then homogenized by three passes through a microfluidizer. The lysed cell suspension was centrifuged in a JA14 rotor at 10,000 rpm for 45 minutes. SDS-PAGE analysis showed a band of approximately 18kd molecular weight present in both inclusion bodies and the supernatant. The soluble fraction was then applied to a Pharmacia SP Sepharose 4FF column equilibrated with 10mM MES pH 6.0. The OPG binding protein was eluted with a 20 column volume gradient of 0-0.4M NaCl in MES pH 6.0. Fractions containing OPG binding protein were then applied to an ABX Bakerbond column equilibrated with 20mM MES pH 6.0. OPG binding protein was eluted with a 15CV gradient of 0-0.5M NaCl in MES pH 6.0. The final product was over 95% homogeneous by SDS-PAGE. N-terminal sequencing gave the following sequence: Met-Lys-Pro-Glu-Ala-Gln-Pro-

Phe-Ala-His which was identified to that predicted for a polypeptide starting at residue 158 (with an initiator methionine). The relative molecular weight of the protein during SDS-PAGE does not change upon reduction.

5

Example 8

In vitro bioactivity of recombinant soluble OPG-bp

10 Recombinant OPG protein has previously been
shown to block vitamin D3-dependent osteoclast formation
from bone marrow and spleen precursors in an osteoclast
forming assay as described in U.S. Serial No.
08/577,788. Since OPG binding protein binds to OPG, and
15 is a novel member of the TNF family of ligands, it is a
potential target of OPG bioactivity. Recombinant
soluble OPG binding protein (158-316), representing the
minimal core TNF α -like domain, was tested for its
ability to modulate osteoclast differentiation from
20 osteoclast precursors. Bone marrow cells were isolated
from adult mouse femurs, and treated with M-CSF. The
non-adherent fraction was co-cultured with ST2 cells in
the presence and absence of both vitamin D3 and
dexamethasone. As previously shown, osteoclasts develop
25 only from co-cultures containing stromal cells (ST2),
vitamin D3 and dexamethasone. Recombinant soluble OPG
binding protein was added at varying concentrations
ranging from 0.16 to 500 ng/ml and osteoclast maturation
was determined by TRAP solution assay and by visual
30 observation. OPG binding protein strongly stimulated
osteoclast differentiation and maturation in a dose
dependent manner, with half-maximal effects in the 1-2
ng/ml range, suggesting that it acts as an potent
inducer of osteoclastogenesis in vitro (Figure 5). The

effect of OPG binding protein is blocked by recombinant OPG (Figure 6).

To test whether OPG binding protein could replace the stroma and added steroids, cultures were established using M-CSF at varying concentrations to promote the growth of osteoclast precursors and various amounts of OPG binding protein were also added. As shown in Figure 6, OPG binding protein dose dependently stimulated TRAP activity, and the magnitude of the stimulation was dependent on the level of added M-CSF suggesting that these two factors together are pivotal for osteoclast development. To confirm the biological relevance of this last observation, cultures were established on bovine cortical bone slices and the effects of M-CSF and OPG binding protein either alone or together were tested. As shown in Figure 7, OPG binding protein in the presence of M-CSF stimulated the formation of large TRAP positive osteoclasts that eroded the bone surface resulting in pits. Thus, OPG binding protein acts as an osteoclastogenesis stimulating (differentiation) factor. This suggests that OPG blocks osteoclast development by sequestering OPG binding protein.

Example 9

In vivo activity of recombinant soluble OPG Binding Protein

Based on in vitro studies, recombinant murine OPG binding protein [158-316] produced in E.coli is a potent inducer of osteoclast development from myeloid precursors. To determine its effects in vivo, male BDF1 mice aged 4-5 weeks (Charles River Laboratories) received subcutaneous injections of OPG binding protein

[158-316] twice a day for three days and on the morning of the fourth day (days 0, 1, 2, and 3). Five groups of mice (n=4) received carrier alone, or 1, 5, 25 or 100µg/ of of OPG binding protein [158-316] per day . An
5 additional 5 groups of mice (n=4) received the above doses of carrier or of OPG binding protein [158-316] and in addition received human Fc-OPG [22-194] at 1mg/Kg/day (approximately 20 µg/day) by single daily subcutaneous injection. Whole blood ionized calcium was determined
10 prior to treatment on day 0 and 3-4 hours after the first daily injection of of OPG binding protein [158-316] on days 1, 2, and 3. Four hours after the last injection on day 3 the mice were sacrificed and radiographs were taken.

15 Recombinant of OPG binding protein [158-316] produced a significant increase in blood ionized calcium after two days of treatment at dose of 5 µg/day and higher (Figure 8). The severity of the hypercalcemia indicates a potent induction of osteoclast activity
20 resulting from increased bone resorption. Concurrent OPG administration limited hypercalcemia at doses of OPG binding protein [158-316] of 5 and 25 µg/day, but not at 100 µg/day. These same animal were analysed by radiography to determine if there were any effects on
25 bone mineral density visible by X-ray (Figure 9). Recombinant of OPG binding protein [158-316] injected for 3 days decreased bone density in the proximal tibia of mice in a dose-dependent manner. The reduction in bone density was particularly evident in mice receiving
30 100 µg/d confirming that the profound hypercalcemia in these animals was produced from increased bone resorption and the resulting release of calcium from the skeleton. These data clearly indicate that of OPG

binding protein [158-316] acts in vivo to promote bone resorption, leading to systemic hypercalcemia, and recombinant OPG abrogates these effects.

5

Example 10

Cloning and Expression of soluble OPG Binding Protein in
mammalian cells

10 The full length clone of murine and human OPG
binding protein can be expressed in mammalian cells as
previously described in Example 2. Alternatively, the
cDNA clones can be modified to encode secreted forms of
the protein when expressed in mammalian cells. To do
15 this, the natural 5' end of the cDNA encoding the
initiation codon, and extending approximately through the
first 69 amino acid of the protein, including the
transmembrane spanning region, could be replaced with a
signal peptide leader sequence. For example, DNA
20 sequences encoding the initiation codon and signal
peptide of a known gene can be spliced to the OPG
binding protein cDNA sequence beginning anywhere after
the region encoding amino acid residue 68. The
resulting recombinant clones are predicted to produce
25 secreted forms of OPG binding protein in mammalian
cells, and should undergo post translational
modifications which normally occur in the C-terminal
extracellular domain of OPG binding protein, such as
glycosylation. Using this strategy, a secreted form of
30 OPG binding protein was constructed which has at its 5'
end the murine OPG signal peptide, and at its 3' end the
human IgG1 Fc domain. The plasmid vector
pCEP4/muOPG[22-401]-Fc as described in U.S. Serial No.
08/577,788, filed December 22, 1995, was digested with
35 NotI to cleave between the 3' end of OPG and the Fc
gene. The linearized DNA was then partially digested

with XmnI to cleave only between residues 23 and 24 of OPG leaving a blunt end. The restriction digests were then dephosphorylated with CIP and the vector portion of this digest (including residues 1-23 of OPG and Fc) was
5 gel purified.

The murine OPG binding protein cDNA region encoding amino acid residues 69-316 were PCR amplified using Pfu Polymerase (Stratagene, San Diego, CA) from the plasmid template using primers the following oligonucleotides:
10 1602-61: CCT CTA GGC CTG TAC TTT CGA GCG CAG ATG

1602-59: CCT CTG CGG CCG CGT CTA TGT CCT GAA CTT TG

The 1602-61 oligonucleotide amplifies the 5' end of the gene and contains an artificial an StuI site. The
15 1602-59 primer amplifies the 3' end of the gene and contains an artificial NotI site. The resulting PCR product obtained was digested with NotI and StuI, then gel purified. The purified PCR product was ligated with vector, then used to transform electrocompetent E. coli
20 DH10B cells. The resulting clone was sequenced to confirm the integrity of the amplified sequence and restriction site junctions. This plasmid was then used to transfect human 293 fibroblasts, and the OPG binding protein-Fc fusion protein was collected from culture
25 media as previously described in U.S. Serial No. 08/577,788, filed December 22, 1995.

Using a similar strategy, an expression vector was designed that is capable of expressing a N-terminal truncation of fused to the human IgG1 Fc domain. This
30 construct consists of the murine OPG signal peptide (aa residue 1-21), fused in frame to murine OPG binding protein residues 158-316, followed by an inframe fusion to human IgG1 Fc domain. To do this, the plasmid vector pCEP4/ murine OPG [22-401] (U.S. Serial No. 08/577,788,
35 filed December 22, 1995), was digested with HindIII and NotI to remove the entire OPG reading frame. Murine OPG

binding protein, residues 158-316 were PCR amplified using from the plasmid template pCDNA/32D-F3 using the following primers:

1616-44: CCT CTC TCG AGT GGA CAA CCC AGA AGC CTG AGG CCC

5 AGC CAT TTG C

1602-59: CCT CTG CCG CCG CGT CTA TGT CCT GAA CTT TG

1616-44 amplifies OPG binding protein starting at residue 158 as well as containing residues 16-21 of the muOPG signal peptide with an artificial XhoI site.

10 1602-59 amplifies the 3' end of the gene and adds an in-frame NotI site. The PCR product was digested with NotI and XhoI and then gel purified.

The Following complimentary primers were annealed to eachother to form an adapter encoding the murine OPG
15 signal peptide and Kozak sequence surrounding the translation initiation site:

1616-41: AGC TTC CAC CAT GAA CAA GTG GCT GTG CTG CGC ACT
20 CCT GGT GCT CCT GGA CAT CA

1616-42: TCG ATG ATG TCC AGG AGC ACC AGG AGT GCG CAG CAC
AGC CAC TTG TTC ATG GTG GA

These primers were annealed, generating 5'
25 overhangs compatible with HindIII on the 5' end and XhoI on the 3' end. The digested vector obtained above, the annealed oligos, and the digested PCR fragment were ligated together and electroporated into DH10B cells. The resulting clone was sequenced to confirm authentic
30 reconstruction of the junction between the signal peptide, OPG binding protein fragment encoding residues 158-316, and the IgG1 Fc domain. The recombinant plasmid was purified, transfected into human 293 fibroblasts, and expressed as a conditioned media product as
35 described above.

Example 11

Peptides of the OPG binding protein and preparation of
5 polyclonal and monoclonal antibodies to the protein

Antibodies to specific regions of the OPG
binding protein may be obtained by immunization with
peptides from OPG binding protein. These peptides may
10 be used alone, or conjugated forms of the peptide may be
used for immunization.

The crystal structure of mature TNF α has been
described [E.Y. Jones, D.I. Stuart, and N.P.C. Walker
(1990) J. Cell Sci. Suppl. 13, 11-18] and the monomer
15 forms an antiparallel β -pleated sheet sandwich with a
jellyroll topology. Ten antiparallel β -strands are
observed in this crystal structure and form a beta
sandwich with one beta sheet consisting of strands
B'BIDG and the other of strands C'CHEF [E.Y. Jones et
20 al., *ibid.*] Two loops of mature TNF α have been
implicated from mutagenesis studies to make contacts
with receptor, these being the loops formed between beta
strand B & B' and the loop between beta strands E & F
[C.R. Goh, C-S. Loh, and A.G. Porter (1991) Protein
25 Engineering 4, 785-791]. The crystal structure of the
complex formed between TNF β and the extracellular domain
of the 55kd TNF receptor (TNF-R55) has been solved and
the receptor-ligand contacts have been described [D.W.
Banner, A. D'Arcy, W. Janes, R. Gentz, H-J. Schoenfeld,
30 C. Broger, H. Loetscher, and W. Lesslauer (1993) Cell
73, 431-445]. In agreement with mutagenesis studies
described above [C.R. Goh et al., *ibid.*] the
corresponding loops BB' and EF of the ligand TNF β were

found to make the majority of contacts with the receptor in the resolved crystal structure of the TNFb:TNF-R55 complex. The amino acid sequence of murine OPG binding protein was compared to the amino acid sequences of TNF α and TNF β . The regions of murine OPG binding protein corresponding to the BB' and EF loops were predicted based on this comparison and peptides have been designed and are described below

5 A. Antigen(s): Recombinant murine OPG
10 binding protein [158-316] has been used as an antigen (ag) for immunization of animals as described below, and serum will be examined using approaches described below. Peptides to the putative BB' and EF loops of murine OPG binding protein have been synthesized and will be used
15 for immunization; these peptides are:

BB' loop peptide: NH₂--NAASIPSGSHKVTLSSWYHDRGWAKIS--COOH
BB' loop-Cys peptide: NH₂--NAASIPSGSHKVTLSSWYHDRGWAKISC--COOH
EF loop peptide: NH₂--VYVVKTSIKIPSSHNLNLM--COOH
20 EF loop-Cys peptide: NH₂--VYVVKTSIKIPSSHNLNLMC--COOH

Peptides with a carboxy-terminal cysteine residue have been used for conjugation using approaches described in section B below, and have been used for immunization.

25 B. Keyhole Limpet Hemocyanin or Bovine Serum Albumin Conjugation: Selected peptides or protein fragments may be conjugated to keyhole limpet hemocyanin (KLH) in order to increase their immunogenicity in animals. Also, bovine serum albumin (BSA) conjugated
30 peptides or protein fragments may be utilized in the EIA protocol. Inject Maleimide Activated KLH or BSA (Pierce Chemical Company, Rockford, IL) is reconstituted in dH₂O to a final concentration of 10 mg/ml. Peptide or protein fragments are dissolved in phosphate buffer then

mixed with an equivalent mass (g/g) of KLH or BSA. The conjugation is allowed to react for 2 hours at room temperature (rt) with gentle stirring. The solution is then passed over a desalting column or dialyzed against
5 PBS overnight. The peptide conjugate is stored at -20°C until used in immunizations or in EIAs.

C. Immunization: Balb/c mice, (Charles Rivers Laboratories, Wilmington, MA) Lou rats, or New Zealand White rabbits will be subcutaneously injected
10 (SQI) with ag (50 µg, 150 µg, and 100 µg respectively) emulsified in Complete Freund's Adjuvant (CFA, 50% vol/vol; Difco Laboratories, Detroit, MI). Rabbits are then boosted two or three times at 2 week intervals with antigen prepared in similar fashion in Incomplete
15 Freund's Adjuvant (ICFA; Difco Laboratories, Detroit, MI). Mice and rats are boosted approximately every 4 weeks. Seven days following the second boost, test bleeds are performed and serum antibody titers determined. When a titer has developed in rabbits,
20 weekly production bleeds of 50 mls are taken for 6 consecutive weeks. Mice and rats are selected for hybridoma production based on serum titer levels; animals with half-maximal titers greater than 5000 are used. Adjustments to this protocol may be applied by
25 one skilled in the art; for example, various types of immunomodulators are now available and may be incorporated into this protocol.

D. Enzyme-linked Immunosorbent Assay (EIA): EIAs will be performed to determine serum antibody (ab)
30 titres of individual animals, and later for the screening of potential hybridomas. Flat bottom, high-binding, 96-well microtitration EIA/RIA plates (Costar Corporation, Cambridge, MA) will be coated with purified recombinant protein or protein fragment (antigen, ag)
35 at 5 µg per ml in carbonate-bicarbonate buffer, pH 9.2

(0.015 M Na_2CO_3 , 0.035 M NaHCO_3). Protein fragments may be conjugated to bovine serum albumin (BSA) if necessary. Fifty μl of ag will be added to each well. Plates will then be covered with acetate film (ICN Biomedicals, Inc., Costa Mesa, CA) and incubated at room temperature (rt) on a rocking platform for 2 hours or over-night at 4°C . Plates will be blocked for 30 minutes at rt with 250 μl per well 5% BSA solution prepared by mixing 1 part BSA diluent/blocking solution concentrate (Kirkegaard and Perry Laboratories, Inc., Gaithersburg, MD) with 1 part deionized water (dH_2O). Blocking solution having been discarded, 50 μl of serum 2-fold dilutions (1:100 through 1: 12,800) or hybridoma tissue culture supernatants will be added to each well. Serum diluent is 1% BSA (10% BSA diluent/blocking solution concentrate diluted 1:10 in Dulbecco's Phosphate Buffered Saline, D-PBS; Gibco BRL, Grand Island, NY)) while hybridoma supernatants are tested undiluted. In the case of hybridoma screening, one well is maintained as a conjugate control, and a second well as a positive ab control. Plates are again incubated at rt, rocking for 1 hour, then washed 4 times using a 1x preparation of wash solution 20x concentrate (Kirkegaard and Perry Laboratories, Inc., Gaithersburg, MD) in dH_2O . Horseradish peroxidase conjugated secondary ab (Boeringer Mannheim Biochemicals, Indianapolis, IN) diluted in 1% BSA is then incubated in each well for 30 minutes. Plates are washed as before, blotted dry, and ABTS peroxidase single component substrate (Kirkegaard and Perry Laboratories, Inc., Gaithersburg, MD) is added. Absorbance is read at 405 nm for each well using a Microplate EL310 reader (Bio-tek Instruments, Inc., Winooski, VT). Half-maximal titre of serum antibody is calculated by plotting the \log_{10} of the serum dilution versus the optical density at 405, then extrapolating at the 50% point of the maximal optical density obtained by

that serum. Hybridomas are selected as positive if optical density scores greater than 5-fold above background. Adjustments to this protocol may be applied; in example, conjugated secondary antibody may
5 be chosen for specificity or non-cross-reactivity.

E. Cell fusion: The animal selected for hybridoma production is intravenously injected with 50 to 100 µg of ag in PBS. Four days later, the animal is sacrificed by carbon dioxide and its spleen collected
10 under sterile conditions into 35 ml Dulbeccos' Modified Eagle's Medium containing 200 U/ml Penicillin G, 200 µg/ml Streptomycin Sulfate, and 4 mM glutamine (2x P/S/G DMEM). The spleen is trimmed of excess fatty tissue, then rinsed through 4 dishes of clean 2x P/S/G DMEM. It
15 is next transferred to a sterile stomacher bag (Tekmar, Cincinnati, OH) containing 10 ml of 2x P/S/G DMEM and disrupted to single cell suspension with the Stomacher Lab Blender 80 (Seward Laboratory UAC House; London, England). As cells are released from the spleen capsule
20 into the media, they are removed from the bag and transferred to a sterile 50 ml conical centrifuge tube (Becton Dickinson and Company, Lincoln Park, NJ). Fresh media is added to the bag and the process is continued until the entire cell content of the spleen is released.
25 These splenocytes are washed 3 times by centrifugation at 225 x g for 10 minutes.

Concurrently, log phase cultures of myeloma cells, Sp2/0-Ag14 or Y3-Ag1.2.3 for mouse or rat splenocyte fusions, respectively, (American Type Culture
30 Collection; Rockville, MD) grown in complete medium (DMEM, 10% inactivated fetal bovine serum, 2 mM glutamine, 0.1 mM non-essential amino acids, 1 mM sodium pyruvate, and 10 mM hepes buffer; Gibco Laboratories, Grand Island, NY) are washed in similar fashion. The
35 splenocytes are combined with the myeloma cells and pelleted once again. The media is aspirated from the

cell pellet and 2 ml of polyethylene glycol 1500 (PEG 1500; Boehringer Mannheim Biochemicals, Indianapolis, IN) is gently mixed into the cells over the course of 1 minute. Thereafter, an equal volume of 2x P/S/G DMEM is slowly added. The cells are allowed to fuse at 37° C for 2 minutes, then an additional 6 ml of 2x P/S/G DMEM is added. The cells are again set at 37°C for 3 minutes. Finally, 35 ml of 2x P/S/G DMEM is added to the cell suspension, and the cells pelleted by centrifugation. Media is aspirated from the pellet and the cells gently resuspended in complete medium. The cells are distributed over 96-well flat-bottom tissue culture plates (Becton Dickinson Labware; Lincoln Park, NJ) by single drops from a 5 ml pipette. Plates are incubated overnight in humidified conditions at 37°C , 5% CO₂. The next day, an equal volume of selection medium is added to each well. Selection consists of 0.1 mM hypoxanthine, 4 x 10⁻⁴ mM aminopterin, and 1.6 x 10⁻² mM thymidine in complete medium. The fusion plates are incubated for 7 days followed by 2 changes of medium during the next 3 days; HAT selection medium is used after each fluid change. Tissue culture supernatants are taken 3 to 4 days after the last fluid change from each hybrid-containing well and tested by EIA for specific antibody reactivity. This protocol has been modified by that in Hudson and Hay, "Practical Immunology, Second Edition", Blackwell Scientific Publications.

While the present invention has been described in terms of the preferred embodiments, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended claims cover all such equivalent variations which come within the scope of the invention as claimed.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid encoding an osteoprotegerin binding protein selected from the group
5 consisting of:

a) the nucleic acid sequence as in Figure 1 (SEQ ID NO:___) and Figure 4 (SEQ ID NO:___);

b) nucleic acids which hybridize to the polypeptide coding regions as shown in Figure 1 (SEQ ID
10 NO:___) and Figure 4 (SEQ ID NO:___) and remain hybridized under high stringency conditions; and

c) nucleic acids which are degenerate to the nucleic acids of (a) or (b).

15 2. The nucleic acid of Claim 1 which is cDNA, genomic DNA, synthetic DNA or RNA.

3. A polypeptide encoded by the nucleic acid of Claim 1.
20

4. The nucleic acid of Claim 1 including one or more codons preferred for Escherichia coli expression.

25 5. The nucleic acid of Claim 1 having a detectable label attached thereto.

6. A nucleic acid encoding a polypeptide comprising the amino acid sequence of residues 1-316 and
30 residues 70-316 as shown in Figure 1 (SEQ ID NO: ___).

7. A nucleic acid encoding a polypeptide comprising amino acid sequence of residues 1-317 and residues 69-317 as shown in Figure 4 (SEQ ID NO:___);
35

8. A nucleic acid encoding a soluble osteoprotegerin binding protein.

9. The nucleic acid of Claim 8 encoding a polypeptide comprising residues 69-317 as shown in Figure 4 (SEQ ID NO:____) and truncations thereof;

10. An expression vector comprising the nucleic acid of Claims 1 and 9.

11. The expression vector of Claim 10 wherein the nucleic acid comprises the polypeptide-encoding region as shown in Figure 1 (SEQ ID NO:____) and Figure 4 (SEQ ID NO:____);

12. A host cell transformed or transfected with the expression vector of Claim 10.

13. The host cell of Claim 12 which is a eucaryotic or procaryotic cell.

14. The host cell of Claim 13 which is Escherichia coli.

15. A process for the production of an osteoprotegerin binding protein comprising:
growing under suitable nutrient conditions host cells transformed or transfected with the nucleic acid of Claim 1; and
isolating the polypeptide product of the expression of the nucleic acid.

16. A polypeptide produced by the process of Claim 15.

17. A purified and isolated osteoprotegerin binding protein, or fragment, analog, or derivative thereof.

5 18. The protein of Claim 17 which is a human osteoprotegerin.

10 19. The protein of Claim 17 having the amino acid sequence as shown in Figure 1 (SEQ ID NO:___) and Figure 4 (SEQ ID NO:___).

20. The protein of Claim 17 which has been covalently modified with a water-soluble polymer.

15 21. The protein of Claim 20 wherein the polymer is polyethylene glycol.

20 22. The protein of Claim 17 which is a soluble osteoprotegerin binding protein.

25 23. The protein of Claim 22 comprising the amino acid sequence from residues 70-316 inclusive as shown in Figure 1 (SEQ ID NO: ___), or a fragment, analog, or derivative thereof.

30 24. The protein of Claim 22 comprising the amino acid sequence from residues 69-317 inclusive as shown in Figure 4 (SEQ ID NO:___) and truncations thereof.

 25. An antibody or fragment thereof which specifically binds an osteoprotegerin binding protein.

35 26. The antibody of Claim 25 which is a monoclonal antibody.

27. A method for detecting the presence of an osteoprotegerin binding protein in a biological sample comprising:

5 incubating the sample with the antibody of Claim 25 under conditions that allow binding of the antibody to the osteoprotegerin binding protein; and detecting the bound antibody.

10 28. A method for detecting the presence of osteoprotegerin in a biological sample comprising:

 incubating the sample with an osteoprotegerin binding protein under conditions that allow binding of the protein to osteoprotegerin; and
15 measuring the bound osteoprotegerin binding protein.

29. A method to assess the ability of a candidate compound to bind to an osteoprotegerin binding protein comprising:

20 incubating the osteoprotegerin binding protein with the candidate compound under conditions that allow binding; and measuring the bound compound.

25 30. The method of Claim 29 wherein the compound is an agonist or an antagonist of an osteoprotegerin binding protein.

30 31. A method of regulating expression of an osteoprotegerin binding protein in an animal comprising administering to the animal a nucleic acid complementary to the nucleic acids as shown in Figure 1 (SEQ ID NO:__) and Figure 4 (SEQ ID NO: ____).

35

32. A pharmaceutical composition comprising a therapeutically effective amount of an osteoprotegerin binding protein in a pharmaceutically acceptable carrier, adjuvant, solubilizer, stabilizer and/or
5 anti-oxidant.

33. The composition of Claim 32 wherein the osteoprotegerin binding protein is a human osteoprotegerin binding protein.
10

34. A method of treating bone disease in a mammal comprising administering a therapeutically effective amount of a modulator of an osteoprotegerin binding protein.
15

35. The method of Claim 34 wherein the modulator is a soluble form of an osteoprotegerin binding protein.

20 36. The method of Claim 35 wherein the modulator is an antibody, or fragment thereof, which specifically binds an osteoprotegerin binding protein.

ABSTRACT OF THE INVENTION

A novel polypeptide, osteoprotegerin binding protein, involved in osteoclast maturation has
5 been identified based upon its affinity for osteoprotegerin. Nucleic acid sequences encoding the polypeptide, or a fragment, analog or derivative thereof, vectors and host cells for production, methods
10 of preparing osteoprotegerin binding protein, and binding assays are also described. Compositions and methods for the treatment of bone diseases such as osteoporosis, bone loss due to arthritis or metastasis, hypercalcemia, and Paget's disease are also provided.

FIGURE 1

| | |
|--|-----|
| GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG | 60 |
| CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CCGTGGGTGG CCGAGGAAGG GAGAGAACGA | 120 |
| TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA | 175 |
| Met Arg Arg Ala Ser Arg | |
| 1 5 | |
| GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC | 223 |
| Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro | |
| 10 15 20 | |
| GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT | 271 |
| Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala | |
| 25 30 35 | |
| CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG | 319 |
| Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser <u>Met Phe Leu Ala Leu Leu</u> | |
| 40 45 50 | |
| GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC | 367 |
| <u>Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr</u> | |
| 55 60 65 70 | |
| TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC | 415 |
| Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His | |
| 75 80 85 | |
| TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC | 463 |
| Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp | |
| 90 95 100 | |
| TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG | 511 |
| Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met | |
| 105 110 115 | |
| AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG | 559 |
| Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val | |
| 120 125 130 | |
| GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG | 607 |
| Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp | |
| 135 140 145 150 | |
| TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC | 655 |
| Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His | |
| 155 160 165 | |
| CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT | 703 |
| Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr | |
| 170 175 180 | |

FIGURE 1 (Con't)

| | |
|--|------|
| CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG | 751 |
| Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser <u>Asn</u> Met | |
| 185 190 195 | |
| ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC | 799 |
| Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr | |
| 200 205 210 | |
| CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA | 847 |
| Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val | |
| 215 220 225 230 | |
| CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC | 895 |
| Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile | |
| 235 240 245 | |
| AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC | 943 |
| Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys <u>Asn</u> | |
| 250 255 260 | |
| TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA | 991 |
| Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly | |
| 265 270 275 | |
| TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC | 1039 |
| Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u> | |
| 280 285 290 | |
| CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC | 1087 |
| Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe | |
| 295 300 305 310 | |
| AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGAACA TTAGCATGGA | 1136 |
| Lys Val Gln Asp Ile Asp | |
| 315 | |
| TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA | 1196 |
| CTAAGAGACA TGGCCACACG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG | 1256 |
| TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTCATG GTGATTACAC AACGGTTTTA | 1316 |
| CAATTTTGTA ATGATTTTCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG | 1376 |
| AAAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT | 1436 |
| GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT | 1496 |
| GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCGCTGGGA CCTGCAAATA AGTTCTTTTT | 1556 |

FIGURE 1 (Con't)

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|------|
| TTCTAATGAG | GAGAGAAAAA | TATATGTATT | TTTATATAAT | GTCTAAAGTT | ATATTTTCAGG | 1616 |
| TGTAATGTTT | TCTGTGCAAA | GTTTGTAA | TTATATTTGT | GCTATAGTAT | TTGATTCAAA | 1676 |
| ATATTTAAAA | ATGTCTCACT | GTGACATAT | TTAATGTTTT | AAATGTACAG | ATGTATTTAA | 1736 |
| CTGGTGCACT | TTGTAATTCC | CCTGAAGGTA | CTCGTAGCTA | AGGGGGCAGA | ATACTGTTTC | 1796 |
| TGGTGACCAC | ATGTAGTTTA | TTTCTTTATT | CTTTTAACT | TAATAGAGTC | TTCAGACTTG | 1856 |
| TCAAAACTAT | GCAAGCAAAA | TAAATAAATA | AAAATAAAAT | GAATACCTTG | AATAATAAGT | 1916 |
| AGGATGTTGG | TCACCAGGTG | CCTTTCAAAT | TTAGAAGCTA | ATTGACTTTA | GGAGCTGACA | 1976 |
| TAGCCAAAAA | GGATACATAA | TAGGCTACTG | AAATCTGTCA | GGAGTATTTA | TGCAATTATT | 2036 |
| GAACAGGTGT | CTTTTTTTTAC | AAGAGCTACA | AATTGTAAAT | TTTGTTTCTT | TTTTTTCCCA | 2096 |
| TAGAAAATGT | ACTATAGTTT | ATCAGCCAAA | AAACAATCCA | CTTTTAAATT | TAGTGAAAGT | 2156 |
| TATTTTATTA | TACTGTACAA | TAAAAGCATT | GTCTCTGAAT | GTTAATTTTT | TGGTACAAAA | 2216 |
| AATAAATTTG | TACGAAAACC | TGAAAAAAAA | AAAAAAAAAA | AAAAAAAGGG | CGGCCGCTCT | 2276 |
| AGAGGGCCCT | ATTCTATAG | | | | | 2295 |

Expression of 32D-F3 in COS-7 Cells

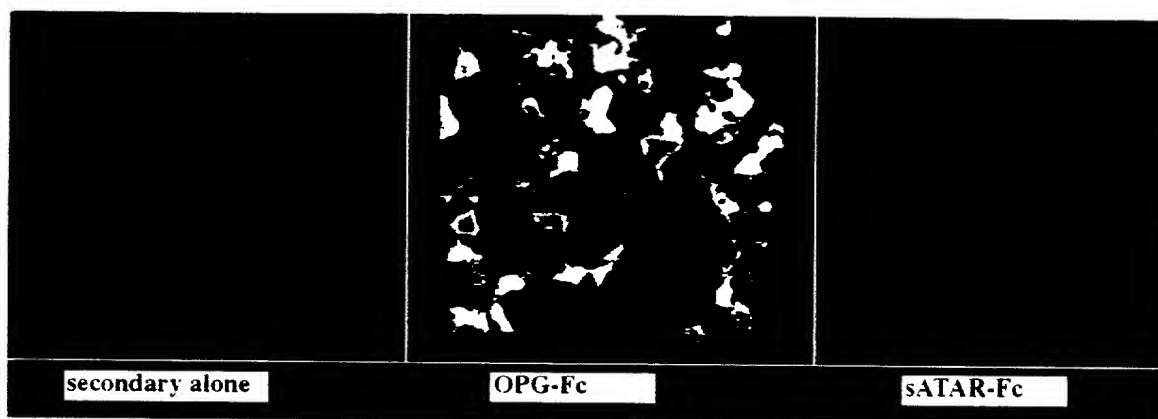


FIGURE 2

OPG Binding Protein Expression in Human Tissues

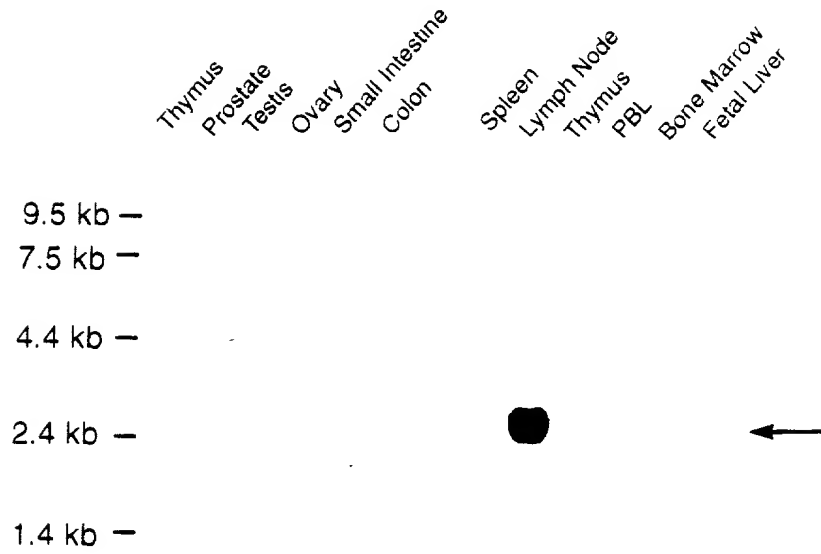


FIGURE 3

FIGURE 4

10 30 50
 AAGCTTGGTACCGAGCTCGGATCCACTACTCGACCCACGCGTCCGCGCGCCCCAGGAGCC
 70 90 110
 AAAGCCGGGCTCCAAGTCGGCGCCCCACGTCGAGGCTCCGCCGACAGCTCCGGAGTTGGC
 130 150 170
 CGCAGACAAGAAGGGGAGGGAGCGGGAGAGGGAGAGCTCCGAAGCGAGAGGGCCGAG
 190 210 230
 CGCCATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGG
 M R R A S R D Y T K Y L R G S E E M G
 250 270 290
 CGGCGGCCCCGGAGCCCCGCACGAGGGCCCCCTGCACGCCCCCGCCGCGCTGCGCCGCA
 G G P G A P H E G P L H A P P P P A P H
 310 330 350
 CCAGCCCCCGCCGCTCCCGCTCCATGTTCTGCGGCCCTCCTGGGGCTGGGGCTGGGCCA
 Q P P A A S R S M F V A L L G L G L G Q
 370 390 410
 GGTGTGTCTGCAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAATAGAAT
 V V C S V A L F F Y F R A Q M D P N R I
 430 450 470
 ATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTT
 S E D G T H C I Y R I L R L H E N A D F
 490 510 530
 TCAAGACACAACCTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATGTAGGAGAAT
 Q D T T L E S Q D T K L I P D S C R R I
 550 570 590
 TAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA
 K Q A F Q G A V Q K E L Q H I V G S Q H
 610 630 650
 CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAA
 I R A E K A M V D G S W L D L A K R S K
 670 690 710
 GCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTC
 L E A Q P F A H L T I N A T D I P S G S
 730 750 770
 CCATAAAGTGAGTCTGTCTCTTGGTACCATGATCGGGGTGGGCCAAGATCTCCAACAT
 H K V S L S S W Y H D R G W A K I S N M
 790 810 830
 GACTTTTAGCAATGGAATACTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAA
 T F S N G K L I V N Q D G F Y Y L Y A N
 850 870 890
 CATTTGCTTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAAT
 I C F R H H E T S G D L A T E Y L Q L M
 910 930 950
 GGTGTACGTCACTAAAACCGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGG
 V Y V T K T S I K I P S S H T L M K G G
 970 990 1010

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FIGURE 4

AAGCACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTTATTCCATAAACGTTGGTGG
S T K Y W S G N S E F H F Y S I N V G G

1030 1050 1070
ATTTTTTAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACT
F F K L R S G E E I S I E V S N P S L L

1090 1110 1130
GGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTTCGAGATATAGATTGAGC
D P D Q D A T Y F G A F K V R D I D

1150 1170 1190
CCCAGTTTTTTGGAGTGTTATGTATTTCTGGATGTTTGGAAACATTTTTTAAACAAGCC

1210 1230 1250
AAGAAAGATGTATATAGGTGTGTGAGACTACTAAGAGGCATGGCCCCAACGGTACACGAC

1270 1290 1310
TCAGTATCCATGCTCTTGACCTTGTAGAGAACACGCGTATTTACAGCCAGTGGGAGATGT

1330 1350 1370
TAGACTCATGGTGTGTACACAATGGTTTTTAAATTTTGTAATGAATTCCTAGAATTAAA

1390 1410 1430
CCAGATTGGAGCAATTACGGGTGACCTTATGAGAACTGCATGTGGGCTATGGGAGGGG

1450 1470 1490
TTGGTCCCTGGTCATGTGCCCCCTCGCAGCTGAAGTGGAGAGGGTGTCTAGCGCAAT

1510 1530 1550
TGAAGGATCATCTGAAGGGGCAAATTCCTTTGAATTGTTACATCATGCTGGAACCTGCAA

1570 1590 1610
AAAATACTTTTTCTAATGAGGAGAGAAAAATATATGTATTTTTTATATAATATCTAAAGTTA

1630 1650 1670
TATTTTCAGATGTAATGTTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT

1690 1710 1730
TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTAAATGTACAGA

1750 1770 1790
CATATTTAACTGGTGCACCTTGTAATTCCTGGGGAAAACCTGCAGCTAAGGAGGGGAA

[illegible][illegible]

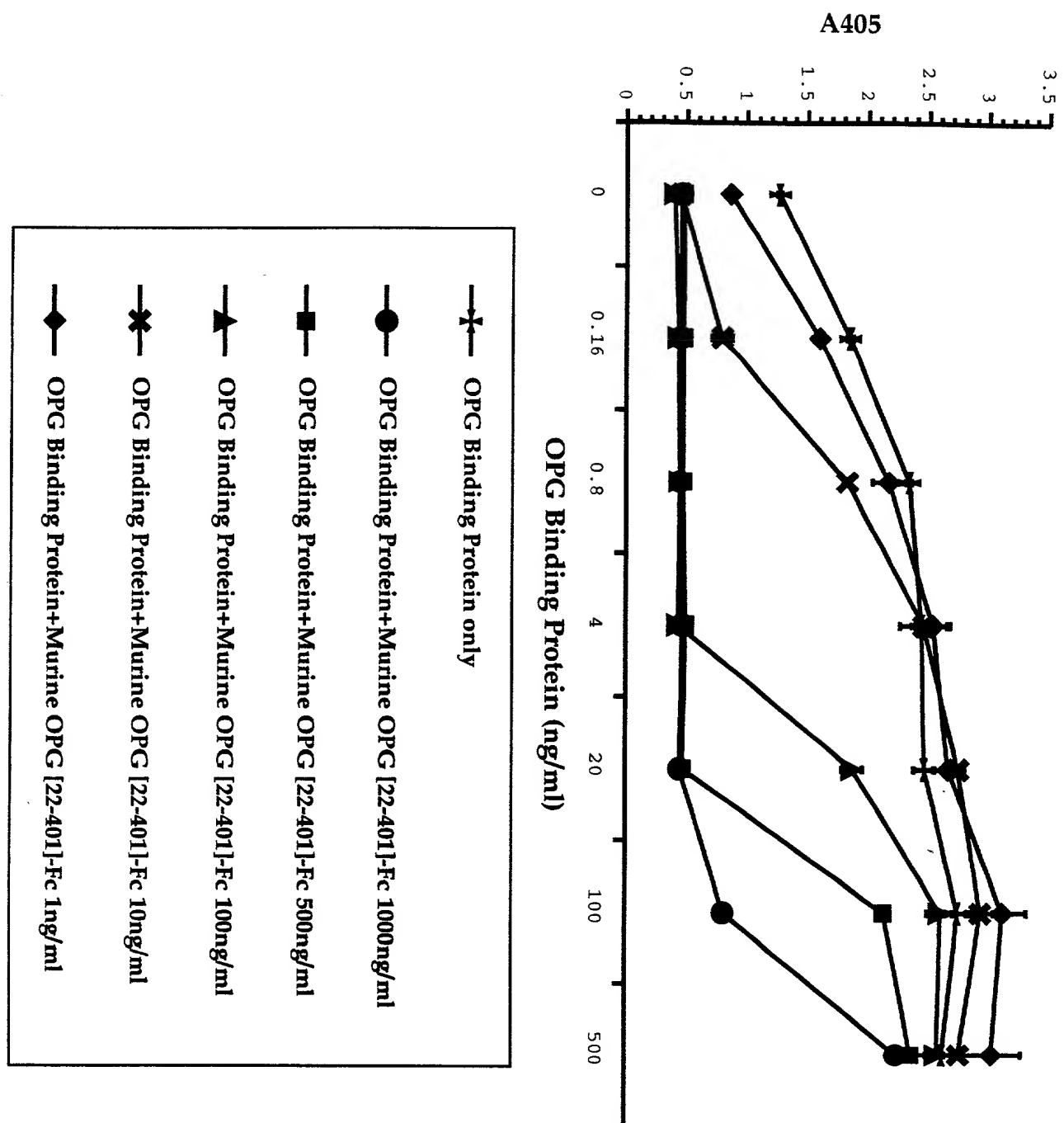
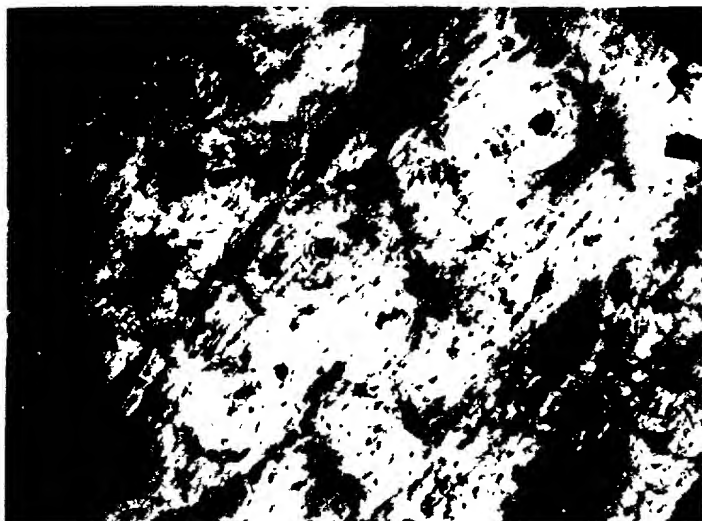
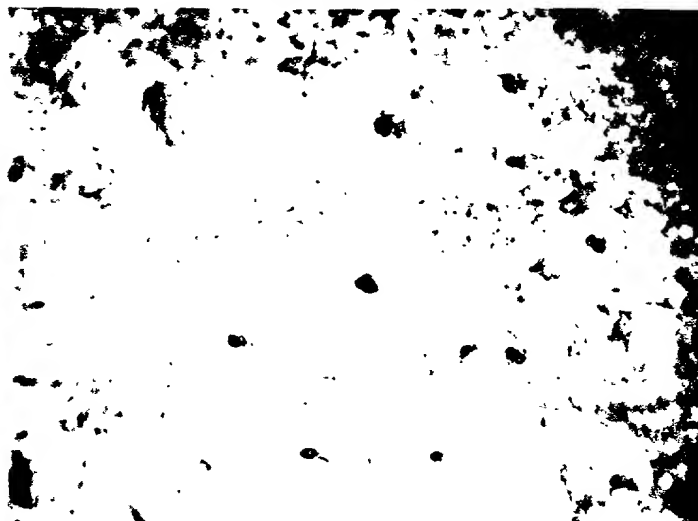


FIGURE 5

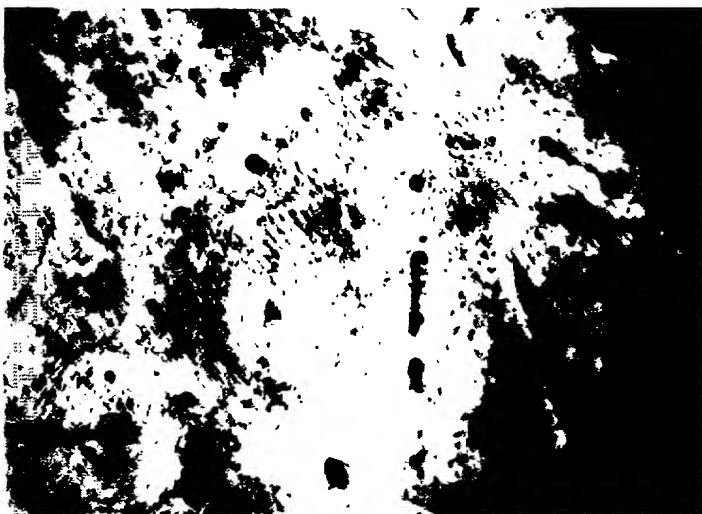
Toluidine Blue Staining



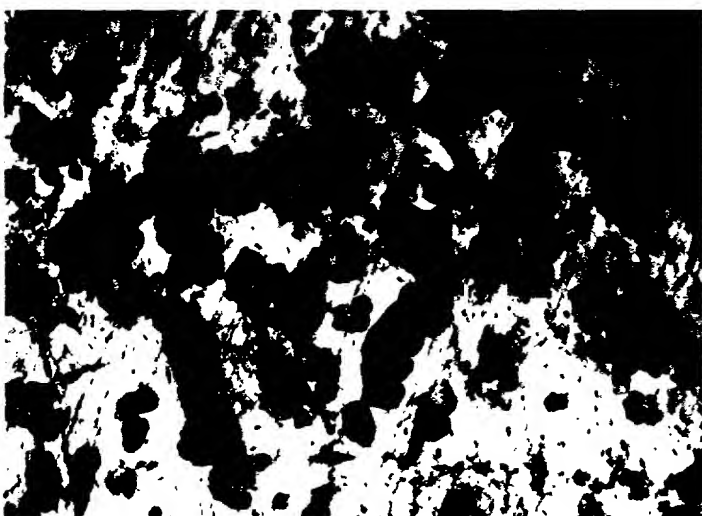
TRAP staining



Bone Marrow Cells + M-CSF-1



Bone Marrow Cells + OPG Binding Protein



Bone Marrow Cells + M-CSF-1 + OPG Binding Protein

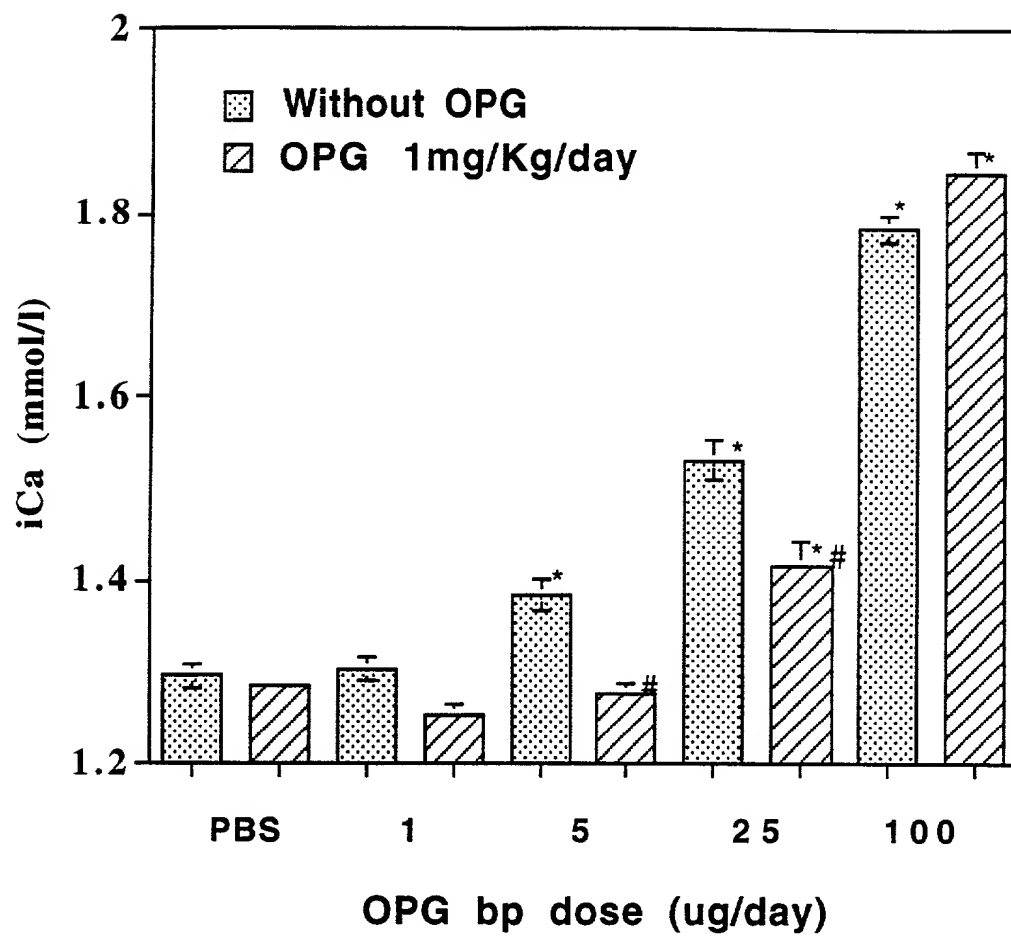


FIGURE 8

PBS



OPGbp 5ug/d



OPGbp 25ug/d



OPGbp100ug/d



FIGURE 9

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first, and sole inventor (if only one name is listed below) or a joint inventor (if plural names are listed below) of the invention entitled

OSTEOPROTEGERIN BINDING PROTEINS

which is described and claimed in the specification which:

- ☒ is attached hereto.
☐ was filed on _____
as Application Serial No. _____
and was amended on _____ (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, § 1.56(a).

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) which occurred between the filing date of the prior application and the filing date of this application:

| APPLICATION SERIAL NO. | FILING DATE | STATUS |
|------------------------|----------------|---------|
| 08/842,842 | April 16, 1997 | Pending |
| | | |
| | | |

Power of Attorney: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith:

Ron K. Levy, Registration No.: 31,539; Steven M. Odre, Registration No.: 29,094; and Robert B. Winter Registration No.:34,458 said attorneys/agents to have in addition full power of revocation, including the power to revoke any power herein granted.

EXPRESS MAIL CERTIFICATE

Express Mail mail labeling number: TB813684146

Date of Deposit: June 23, 1997

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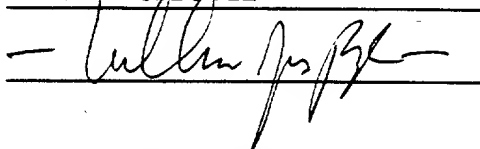
Robert B. Winter
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Registration No.: 34,458
Phone: (805) 447- 2425
Date: June 23, 1997

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Full Name of Sole
or First Inventor:

WILLIAM J. BOYLE

Inventor's Signature:



Date:

6.23.97

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